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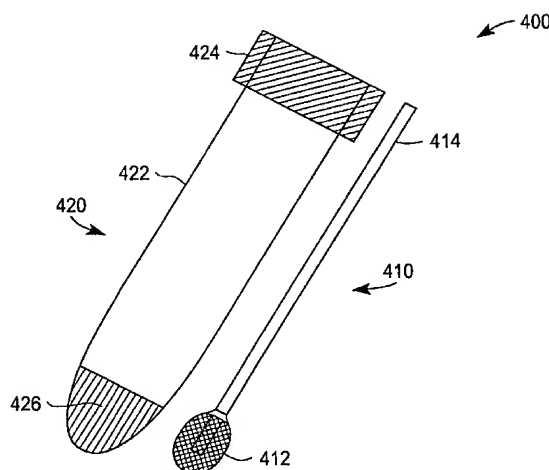
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(54) Title: DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION OF COLORECTAL
CANCER: REAGENTS, METHODS AND KITS THEREOF



(57) Abstract: A novel approach to the early detection of colorectal cancer ("CRC"), using a molecular diagnostic test to evaluate grossly normal-appearing colonic tissue for the early detection of colorectal cancer is disclosed. Such grossly normal-appearing colonic mucosal cells may be collected from non-invasive or minimally invasive procedures. The use of novel biomarker panels for drug screening also is disclosed. Such biomarker panels may be used wholly or in part as surrogate endpoints for monitoring effectiveness of a prospective drug in the intervention of pathologies, such as cancers, for example CRC, lung, prostate, and breast, and neurodegenerative diseases, for example Alzheimer's and ALS.



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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

**DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION OF COLORECTAL
CANCER: REAGENTS, METHODS, AND KITS THEREOF**

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Claim of Priority

U.S. Provisional Patent Application No. 60/614,746 entitled MOLECULAR
DIAGNOSTIC TEST FOR EARLY DETECTION OF COLORECTAL CANCER: REAGENTS,
METHODS, AND KITS THEREOF, by Nancy M. Lee, *et al.*, filed September 30, 2004
(Attorney Docket No. NLEE-01001US0);

10

U.S. Provisional Patent Application No. 60/651,344 entitled METHODS OF USE OF
A BIOMARKER PANEL FOR DRUG SCREENING, by Nancy M. Lee, *et al.*, filed February 8,
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15

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CANCER: REAGENTS, METHODS, AND KITS THEREOF, by Nancy M. Lee, filed
September 29, 2005 (Attorney Docket No. NLEE-01001US1).

Cross-Reference to Related Applications

20

This application is related to PCT/US2004/022594, entitled "Biomarker Panel for
Colorectal Cancer," by Nancy M. Lee et al., filed July 14, 2004 (Attorney Docket No. NLEE-
01000WO0), which claims priority to U.S. Provisional Application No. 60/488,660, entitled
"Molecular Biomarker Panel for Determination of Colorectal Cancer," by Nancy M. Lee et al.,
filed July 18, 2003 (Attorney Docket No. CPMC-01000US0), and also to U.S. Patent
Application No. 10/690,880, entitled "Biomarker Panel for Colorectal Cancer," by Nancy M.
Lee et al., filed October 22, 2003 (Attorney Docket No. CPMC-01000US1), each of which is
incorporated herein in full, by reference.

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Nucleotide and/or amino acid sequence listings are included in this application in
computer-readable form and in hard-copy. The information included in computer-readable
form is incorporated herein in full by reference. The information in computer-readable form
is also included on diskette, and such information submitted on diskette is incorporated
herein in full by reference. Compact diskette No. 1 contains the following file:
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is one.

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Background

The field of art of this disclosure concerns reagents, methods, and kits for the early detection of colorectal cancer ("CRC"), and methods for drug screening effective in the treatment of pathologies, such as cancers, for example, CRC, lung, prostate, and breast, and neurodegenerative diseases, for example Alzheimer's and ALS. These reagents, methods, and kits are based on a panel of biomarkers that are useful for risk assessment, early detection, establishing prognosis, evaluation of intervention, recurrence of CRC and other such pathologies, and drug discovery for therapeutic intervention.

In the field of medicine, clinical procedures providing for the risk assessment and early detection of CRC have been long sought. Currently, CRC is the second leading cause of cancer-related deaths in the Western world. One picture that has clearly emerged through decades of research into CRC is that early detection is critical to enhanced survival rates.

Thus, one long-sought approach for the early detection of CRC has been the search for biomarkers that are effective in the early detection of CRC, and therefore that are effective for the treatment of CRC. For more than four decades, since the discovery of carcinogenic embryonic antigen ("CEA"), the search for biomarkers effective for early detection of CRC has continued. It is further advantageous for sampling methods used in conjunction with an early diagnostic test for CRC to be minimally invasive or non-invasive. Non-invasive and minimally invasive sampling methods increase patient compliance, and generally reduce cost. Additionally, bioinformatic methods for analysis of complex, multivariate data typical of bioanalysis, yielding a reliable diagnostic evaluation based on such data sets, are also desirable.

Therapeutic intervention for numerous types of cancers, such as CRC, lung, prostate, and breast, includes surgery, chemotherapy, and radiation treatment, and combinations thereof. For CRC, a current area of continued research and development, in addition to search for non-invasive methods for early detection, is in the area of drug development.

One picture that has clearly emerged through decades of research into CRC is that early detection, coupled with effective therapeutic intervention is critical to enhanced survival rates. To date, the most commonly used drug in the treatment of CRC is 5-fluoruracil ("5FU"), which frequently is administered intravenously, in combination with the folic acid vitamin, leucovorin. A strategy referred to as primary chemotherapy is used when metastasis has occurred, and the cancer has spread to different parts of the body. For CRC, the current strategy for primary chemotherapy is the administration of an oral form of

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5FU, capecitabine, in combination with Camptosar, a topoisomerase I inhibitor, or Eloxatin, an organometallic, platinum-containing drug that inhibits DNA synthesis.

Currently, strategies for new drug development for CRC include two areas of research: angiogenesis inhibitors, and signal transduction inhibitors.

5 Novel biopharmaceutical drugs include both protein- and ribozyme-based therapeutics. Humanized antibody-based therapeutics include examples such as Erbitux and Avastin. Erbitux, a signal transduction inhibitor, is aimed at inhibiting epidermal growth factor receptors ("EGFR") on the surface of cancerous cells. Avastin, an angiogenesis inhibitor, is aimed at inhibiting vascular endothelial growth factor ("VEGF"), which is known
10 to promote the growth of blood vessels. Additionally, Angiozyme, an example of a ribozyme-based therapeutic, is an angiogenesis inhibitor directed against the expression of the VEGF-R1 receptor. New traditional small molecule-based drugs include examples such as Iressa, based on a quinazoline template, and acting as a signal transduction inhibitor, and SU11248, based on an indolinone template, which acts as an anti-angiogenesis
15 inhibitor.

Still, a number of potential drawbacks and uncertainties remain for these nascent drug therapies for CRC. In addition to typical contraindications such as nausea, vomiting, headache, and diarrhea, other more serious side effects, such as gastrointestinal perforation, elevated or lowered blood pressure, extreme fatigue, and internal bleeding have
20 been observed for many of the promising candidates. Additionally, though many of the drug therapies based on angiogenesis inhibition or signal transduction inhibition appear promising, they are in the very early stages of clinical trials.

Accordingly, a need exists in the art for biomarkers that are effective in the early detection of CRC, coupled with sampling methods that are minimally or non-invasive, and
25 bioinformatic methods, which together produce a robust diagnostic test for the early detection of CRC. A need also exists in the art for drug development, which can provide effective treatment prior to the development of cancer for individuals diagnosed with pathologies, such as cancers, for example CRC, lung, prostate, and breast, and neurodegenerative diseases, for example Alzheimer's and ALS, while minimizing serious
30 side effects.

Brief Description of Figures

Fig. 1 is a table listing an embodiment of sequence listings for a panel of biomarkers of the disclosed invention.

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Fig. 2 is a distribution plot of control subjects versus test subjects evaluated using an aspect of the panel of biomarkers of **Fig. 1**, and an aspect of a bioinformatic evaluation of the disclosed invention.

Fig. 3 shows the distribution of the log (base2) expression values for genes, PPAR- γ , IL-8, SAA 1 and COX-2 and their cut-off points.

Figs. 4A and 4B show that expression of different genes is altered at different sites of MNCM from individuals with a family history of colon cancer.

Fig. 5 displays a flow diagram of an aspect of the bioinformatic process used for evaluating data.

Fig. 6 is an embodiment of a swab sampling and transport system for the minimally invasive sampling of colonic mucosal cells.

Fig. 7 is a flow chart depicting one aspect of the drug screening disclosure.

Fig. 8 is a flow chart depicting another aspect of the drug screening disclosure.

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Detailed Description

To date, a greater understanding of the biology of CRC has been gained through the research on adenomatous polyposis coli ("APC"), p53, and Ki-ras genes, as well as the corresponding proteins, and related pathways involved regulation thereof. However, there is a distinct difference between research on a specific gene, its expression, protein product, and regulation, and understanding what genes are critical to include in a panel used for the analysis of CRC that is useful in the management of patient care for the disease. Panels that have been suggested for CRC are comprised of specific point mutations of the APC, p53, and Ki-ras, as well as BAT-26, which is a gene that is a microsatellite instability marker.

For CRC, biomarkers for risk assessment and early detection of CRC long have been sought. The difference between risk assessment and early detection is the degree of certainty regarding acquiring CRC. Biomarkers that are used for risk assessment confer less than 100% certainty of CRC within a time interval, whereas biomarkers used for early detection confer an almost 100% certainty of the onset of the disease within a specified time interval. Risk factors may be used as surrogate end points for individuals not diagnosed with cancer, providing that there is an established relationship between the surrogate end point and a definitive outcome. An example of an established surrogate end point for CRC is the example of adenomatous polyps. What has been established is that the occurrence of adenomatous polyps is a necessary, but not sufficient condition for an individual later to develop CRC. This is demonstrated by the fact that 90% percent of all preinvasive

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cancerous lesions are adenomatous polyps or precursors, but not all individuals with adenomatous polyps go on later to develop CRC.

Adenomatous polyps have been established as surrogate end points for CRC, and adenomatous polyps are macroscopically identifiable by colonoscopy or sigmoidoscopy.

5 During such invasive procedures, biopsy samples can be taken from polyps or lesions for histological evaluation of the tissue. The molecular diagnostic approach disclosed herein may be used on grossly normal-appearing colonic mucosal cells that are not from a macroscopically identifiable polyp or lesion. However, as further disclosed herein, an invasive procedure need not be used to obtain a patient sample for histological evaluation.

10 A non-invasive or minimally-invasive procedure can be employed to obtain, for example, a blood sample, stool sample, or swab of grossly normal-appearing rectal cells, upon which a molecular diagnostic test can be performed to evaluate the presence or absence of CRC. No previously-described approach for early detection of CRC has disclosed the non-invasive or minimally invasive collection of grossly normal-appearing colonic mucosal cells (biopsy or

15 swab of rectal cells), blood samples, and/or stool samples, followed by a molecular and/or protein expression diagnostic test, which can detect changes in the tissue before any untoward histological changes indicating CRC are manifest.

Fig. 1 is a table that gives an overview of the sequence listings included with this disclosure. The table of **Fig. 1** lists a panel of biomarkers useful in practicing the disclosed

20 invention. One embodiment of a biomarker panel is the 16 identified coding sequences given by SEQ. ID NOs 1-16, while another embodiment of a biomarker panel is the 16 identified proteins given by SEQ. ID NOs 17-32. These two embodiments represent molecular marker panels that provide the selectivity and sensitivity necessary for the early detection of CRC. It is to be understood that fragments and variants of the biomarkers

25 described in the sequence listings are also useful biomarkers in embodiments of panels used for the early detection of CRC. What is meant by fragment is any incomplete or isolated portion of a polynucleotide or polypeptide in the sequence listing. Further, it is recognized that almost daily, new discoveries are announced for gene variants, particularly for those genes under intense study, such as genes implicated in diseases like cancer.

30 Therefore, the sequence listings given are exemplary of what now is reported for a gene, but it is recognized that for the purpose of an analytical methodology, variants of the gene and their fragments also are included.

In **Fig. 1**, the entries 1-16 in the table are one aspect of a panel of biomarkers, which are polynucleotide coding sequences, and include the name and abbreviation of the gene.

35 Entries 17-32 in **Fig. 1** are another embodiment of a panel of biomarkers, which are protein,

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or polypeptide, amino acid sequences that correspond to the coding sequences for entries 1-16. A biomarker, as defined by the National Institutes of Health ("NIH") is a molecular indicator of a specific biological property; a biochemical feature or facet that can be used to measure the progress of disease or the effects of treatment. A panel of biomarkers is a selection of biomarkers, which taken together can be used to measure the progress of disease or the effects of treatment. Biomarkers may be from a variety of classes of molecules. As previously mentioned, there remains a need for biomarkers for CRC having the selectivity and sensitivity required to be effective for early detection of CRC. Therefore, one embodiment of what is disclosed herein is the selection of an effective set of biomarkers that is differentiating in providing the basis for early detection of CRC.

In one aspect of this disclosure, for the early detection of CRC, expression levels of polynucleotides indicated as SEQ. ID NOs 1-16 are determined from cells in samples taken from patients by non-invasive or minimally invasive methods. The contemplated methods include blood sampling, stool sampling, and rectal cell swabbing or biopsy. Such analysis of polynucleotide expression levels frequently is referred to in the art as gene expression profiling. For gene expression profiling, levels of mRNA in a sample are measured as a leading indicator of a biological state -- in this case, as an indicator of CRC. One of the most common methods for analyzing gene expression profiling is to create multiple copies from mRNA in a biological sample (said sample taken from a patient as disclosed above, by non- or minimally-invasive methods) using a process known as reverse transcription. In the process of reverse transcription, the mRNA from the sample is isolated from cells in the biological sample, by methods well-known in the art. The mRNA then is used to create copies of the corresponding DNA sequence from which the mRNA was originally transcribed. In the reverse transcription amplification process, copies of DNA are created without the regulatory regions in the gene (*i.e.*, introns). These multiple copies made from mRNA are therefore referred to as "cDNA," which stands for complementary, or copy DNA. Entries 33-64 are the sets of primers that can be used in the reverse transcription process for each biomarker gene listed in entries 1-16. All nucleotide and amino acid biomarker sequences identified in SEQ. ID NOs 1-64 are found in a printout attached and included as subject matter of this application, and are found on a diskette also included as part of this application and incorporated herein by reference.

Since the reverse transcription procedure amplifies copies of cDNA proportional to the original level of mRNA in a sample, it has become a standard method that allows the identification and quantification of even low levels of mRNA present in a biological sample.

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Genes either may be up-regulated or down-regulated in any particular biological state, and hence mRNA levels shift accordingly.

In one aspect of this disclosure, a method for gene expression profiling comprises the quantitative measurement of cDNA levels for at least two of the biomarkers of the panel of biomarkers selected from SEQ. ID NOs. 1-16, in a biological sample taken from a patient by a non- or minimally-invasive procedure, such as blood sampling, stool sampling, rectal cell swabbing, and/or rectal cell biopsy. The tissue taken need not be apparently diseased; in fact, the disclosed invention is contemplated to be useful in evaluating even grossly normal-appearing cells for detection of CRC. Such a method for gene expression profiling requires the use of primers, enzymes, and other reagents for the preparation, detection, and quantifying of cDNAs. The method of creating cDNA from mRNA in a sample is referred to as the reverse transcriptase polymerase chain reaction ("RT-PCR"). The primers listed in SEQ. ID NOs 33-64 are particularly suited for use in gene expression profiling using RT-PCR based on the disclosed biomarkers in the biomarker panel. A series of primers were designed using Primer Express Software (Applied Biosystems, Foster City, CA). Specific candidates were chosen, and then tested to verify that only cDNA was amplified, and not contaminated by genomic DNA. The primers listed in SEQ. ID NOs 33-64 were specifically designed, selected, and tested accordingly.

The primers listed in SEQ. ID NOs 33-64 are important in the step subsequent to creating cDNA from isolated cellular RNA, for quantitatively amplifying copies in the real time PCR of gene expression products of interest. Optimal primer sequence, and optimal primer length are key considerations in the design of primers. The optimal primer sequence may impact the specificity and sensitivity of the binding of the primer with the template. A primer length between 18-30 bases is considered an optimal range. Theoretically, 18 bases is the minimal length representing a unique sequence, which would hybridize at only one position in most eukaryotic genomes. The primers listed in SEQ. ID NOs 33-64 range in primer length between 21-27 bases, and were designed and validated to amplify cDNA for the panel of nucleotides selected from SEQ. ID NOs 1-16. The specificity of the primers was demonstrated by a single product on 10% polyacrylamide gel electrophoresis ("PAGE"), and a single dissociation curve of the PCR product.

Once the primer pairs have been designed, and validated for specificity, they may be synthesized in large quantities, and stored for convenient future use. Since the PCR reaction is sensitive to buffer concentration and buffer constituents, primers should be maintained in a suitable diluent that will not interfere in the amplification reaction. One example of a suitable diluent is 10 mM Tris buffer, with or without 1mM EDTA, depending on

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the assay sensitivity to EDTA. Alternatively, another example of a suitable diluent for the primers is deionized water that is nuclease-free. The primers may be aliquoted in appropriate containers, such as siliconized tubes, and lyophilized if so desired. The liquid or lyophilized samples are preferably stored at refrigeration temperatures defined as long-term for biological samples, which is between about -20C° to about -70C°. The concentration of primer in the amplification reaction is typically between 0.1 to 0.5 μ M. The typical dilution factor from the stock solution to the final reaction mixture is about 10 times, so that the aliquoted stock solution of the primers is typically between about 1 and 5 μ M.

In addition to the specifically designed primers listed in SEQ. ID Nos. 33-64, reagents such as one including a dinucleotide triphosphate mixture having all four dinucleotide triphosphates (e.g., dATP, dGTP, dCTP, and dTTP), one having the reverse transcriptase enzyme, and one having a thermostable DNA polymerase, are required for RT-PCR. Additionally buffers, inhibitors, and activators also are required for the RT-PCR process.

Fig. 2 depicts one aspect of a bioinformatic data reduction process used for the early detection of CRC, showing a distribution of Mahalanobis distance for 17 controls (left), compared with 14 individuals with family history of CRC (middle), and 24 individuals with polyps (right). Tissue samples taken from grossly normal-appearing colonic mucosal tissue were evaluated using the biomarker panel of polynucleotides selected from SEQ. ID NOs. 1-16. The means for the gene expression levels for each of the 16 genes represented by polynucleotides selected from SEQ. ID NOs 1-16 for each control and test subject were calculated in log base 2 domain. The multivariate means, in a 16 dimensional hyperspace, were then determined for the controls, based on a multivariate normal distribution, in order to establish limits of normal expression levels. For each control, the Mahalanobis distance ("M-dist") from the multivariate mean of the other 16 controls was measured, while the M-dist for each of the test subjects was determined from the multivariate mean of the 17 controls. In each group displayed in **Fig. 2**, all the biopsies from a single individual form a vertical row. For the individuals with polyps, astericks mark the biopsies from individuals with hyperplastic polyps. The horizontal line indicates the 95th percentile of a chi-square distribution with 16 degrees of freedom. All values above this line (corresponding to an M-dist of about 25) are different from the mean of controls at a level of $p < 0.05$. The data presented clearly show that there is an altered gene expression pattern in grossly normal colonic mucosal tissue samples for the test subjects. The data accordingly demonstrate the enhanced sensitivity and selectivity of a diagnostic test using the biomarker panel of polynucleotides selected from SEQ. ID NOs. 1-16.

Fig. 3 displays a flow diagram **300** of an aspect of the bioinformatic process used for evaluating the data from samples analyzed using expression profiling of polynucleotides selected from SEQ. ID Nos. 1-16. The goal of the bioinformatic analysis used to analyze the gene expression data for the molecular diagnostic test using the panel of polynucleotides selected from SEQ. ID NOs 1-16 was to use a single, easy-to-calculate measure of abnormality. It is desirable to analyze expression patterns of all genes in the panel selected from SEQ. ID NOs 1-16 by multivariate analysis, since multivariate analysis determines the significance of changes of all expression levels, taken together. There are several kinds of multivariate tests which may be useful for the bioinformatic analysis used to assess the presence or absence of colorectal cancer in patient samples tested using the molecular diagnostic test disclosed herein. Examples of multivariate analysis tests useful in the assessment of data from patient samples tested using the panel of polynucleotide biomarkers selected from SEQ. ID NOs 1-16 include the ANOVA and the Mahalanobis distance ("M-Dist") tests.

ANOVA is a global test that accounts for correlations among expression levels. It is desirable for the multivariate ANOVA tests to be based on Wilks' lambda criterion and to be carried out on log(base 2) values for the data obtained using the molecular diagnostic test using the panel of polynucleotides selected from SEQ. ID NOs 1-16 to achieve normal distribution of values.

M-dist analysis is another example of a multivariate analysis that summarizes, in a single number, the differences between two patterns of gene expression, taking into account variability of each gene's expression and correlations among pairs of genes. M-dist is often used as a test for outliers (individual cases that are significantly different from all other individual cases in the group) in multivariate data. M-dist can be converted to p-values by reference to a chi-square distribution with degrees of freedom equal to the number of variables (*i.e.*, genes). However, to avoid reliance on an assumption of multivariate normality, it is desirable to compare M-dist for individual cases (*i.e.*, those with polyps) to controls using a rank sum test, the Mann-Whitney test. By using the Mann-Whitney analysis, the inferences concerning differences in expression patterns do not depend on the assumption of multivariate normality. Therefore, this method allows the determination of the significance of all the experimental subjects' expression levels taken together, as well as the significance of each individual expression value.

A working example of the foregoing disclosure is provided below. Hao, C-Y, et al., *Alteration of Gene Expression in Macroscopically Normal Colonic Mucosa from Individuals with a Family History of Sporadic Colon Cancer*, 11 Clin. Cancer Res., 1400-07 (Feb. 15,

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2005). The example presented is provided as a further guide to the practitioner of ordinary skill in the art, and is not to be construed as limiting the invention in any way.

This example was undertaken to investigate whether expression of several genes was altered in morphologically normal colonic mucosa ("MNCM") of individuals who have not developed colon cancer, but are at high risk of doing so because of a family history of CRC.

Human subjects

Biopsies of MNCM from the rectum and sigmoid colon were performed at the time of routine colonoscopy from individuals seen at the California Pacific Medical Center ("CPMC") who had no history of prior colon cancer, and who were free of adenomatous polyps, colon cancer or other colonic lesions at the time of examination. Twelve individuals with a family history of colon cancer in a first-degree relative (Table 3) and sixteen individuals with no known family history of colon cancer were included in the study. Although the information of family cancer history is obtained by patients' self-reports without confirmation from the hospital's cancer registry, a recent study has confirmed the accuracy of self-reported family history with regard to colon cancer. Of the twelve individuals with a family history of colon cancer, two are mother and daughter (cases #6 and 7 in Table 3), two are sister and brother (cases #11 and 12), and the rest are not related. Study subjects ranged in age from 18 to 64 years in the group with a family history of colon cancer, and 16 to 83 years in the control group (the 16-year-old had undergone colonoscopy for chronic abdominal pain). The research protocols for obtaining normal biopsy specimens for study were approved by the CPMC Institutional Review Board. The appropriate procedure for obtaining informed consent was followed for all study subjects.

Extraction and preparation of RNA and cDNA

Biopsy samples obtained from the segment of colon between the cecum and the hepatic flexure were classified as ascending colon samples; those from the segment of colon between the hepatic flexure and the splenic flexure as transverse colon samples; those from the segment of colon below the splenic flexure as descending colon; those from the winding segment of colon below the descending colon were classified as rectosigmoid colon samples (approximately 5-25 cm from rectum). The number of biopsy samples obtained from each patient varied. Two to eight biopsy samples were obtained from each colon segment, except that only one sample was obtained from the transverse and the descending colon segments in one subject of the family history group. A total of 39 ascending colon, 37 transverse colon, 45 descending colon and 77 rectosigmoid specimens were obtained from the 12 individuals with a family history of colon cancer; and a total of 53 ascending colon, 48 transverse colon, 49 descending colon and 104 rectosigmoid

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specimens were obtained from the 16 individuals with no family history of colon cancer. All biopsy samples were snap-frozen on dry ice and taken immediately to the laboratory for RNA preparation and reverse transcription as described.

Analysis of gene expression

5 The expression levels of oncogene c-myc, CD44 antigen ("CD44"), cyclooxygenase 1 and 2 ("COX-1" and "COX-2"), cyclin D1, cyclin-dependent kinase inhibitor ("p21^{cip/waf1}"), interleukin 8 ("IL-8"), interleukin 8 receptor ("CXCR2"), osteopontin ("OPN"), melanoma growth stimulatory activity ("Gro α /MGSA"), GRO3 oncogene ("Gro γ "), macrophage colony stimulating factor 1 ("MCSF-1"), peroxisome proliferative activated receptor, alpha, delta and
10 gamma ("PPAR- α , δ and γ ") and serum amyloid A 1 ("SAA 1") were analyzed by quantitative RT-PCR. Quantitative RT-PCR were carried out. In brief, the cycle numbers ("C_T value") were recorded when the accumulated PCR products crossed an arbitrary threshold. To normalize this value, a ΔC_T value was determined as the difference between the C_T value for each gene tested and the C_T value for β -actin. The average ΔC_T value for each gene in
15 the control group was calculated. The $\Delta\Delta C_T$ value was determined as the difference between the ΔC_T value for each individual sample and the average ΔC_T value for this gene obtained from the control samples. These $\Delta\Delta C_T$ values were then used to calculate relative gene expression values as described. (Applied Biosystems, User Bulletin #2, December 11, 1997). All PCR were performed in duplicate when cDNA samples were available. The
20 results were also verified using histidyl-tRNA synthetase as internal control. Relative gene expression values yielded similar results using either β -actin or his-tRNA synthetase as a reference. Statistical analyses reported here were obtained using β -actin as normalization controls.

Statistical analysis

25 Gene expression patterns were compared between individuals with a family history of colon cancer and the control group subjects who had no family history of colon cancer. Rather than testing expression of each gene separately and adjusting for multiple comparisons by methods that reduce statistical power, we tested the expression patterns of all genes by multivariate analysis of variance ("MANOVA") with Wilks' lambda criterion. This
30 test is a multivariate analog of the F-test for univariate analysis of variance, which tests the equality of means. This type of analysis takes into account correlations among gene expression levels and controls the false-positive rate by providing a single test of whether the expression patterns, based on all the genes in the subset, differ between groups.

 If there was evidence that expression patterns differed between groups, we used
35 univariate t-tests to determine which genes were contributing to the global difference. All

MANOVA tests were based on the Wilks' lambda criterion and were carried out on log (base 2) of the expression levels, since this transformation was required to achieve normal distributions. Our data consisted of a variable number of samples per subject with different numbers of individuals per group (family history vs. no family history). The analysis included

5 random effects terms for individuals within group and for samples within individuals to account for the sampling scheme. If Y_{ijk} denotes a log2 gene expression value for the k^{th} sample from the j^{th} patient from the i^{th} group, the statistical model is described mathematically by the equation: $Y_{ijk} = M + A_i + B_{ij} + e_{ijk}$, where A_i is the (fixed) group effect, B_{ij} is the (random) patient effect, and e_{ijk} is the (random) sample within patient effect.

10 We also tested whether or not the magnitude of the differential expression (over or under expression) increased along the colon from the ascending portion toward rectum, by defining a variable with value 1 for samples from the ascending, 2 for samples from the transverse, 3 for samples from the descending and 4 for samples from the rectosigmoid portion of the colon. This variable was added to the model so that its effect could be tested

15 for certain genes using univariate ANOVA.

Definition of cut-off point

The log (base 2) of the expression levels of all the biopsy samples from the control group was used to calculate the cut-off point for either up-regulation or down regulation of each gene. A table of tolerance bounds for a normal distribution was used to define cut-off

20 points so that a fraction of the distribution of no more than P would lie above the cut-off point for up-regulated genes or below the cut-off point for down-regulated genes. Each cut-off point was defined by cut-off point = mean + $k(\text{SD})$, where the mean and SD (Standard Deviation) are based on values from the control group. Values of k are found in the table and depend on the P value and the number of normal samples. Owen, D.B., Noncentral t

25 and tolerance limits, in Brimbaum ZW, ed. Handbook of Statistical Tables, Reading, MA: Addison-Wesley, 1962, 108-127. Assuming a Gaussian distribution of expression levels of each gene, one would expect less than 1% of the biopsies from a normal population to have an expression level exceeding the 99% tolerance limit ($p = 0.01$).

To calculate the probability that the number of observed samples outside the upper

30 99 percentile was due to chance in each case, we used the binomial distribution method with $p = 0.01$ and n = the number of samples for each case multiplied by the number of genes tested. For example, for case #1 (Table 3) we had 2 samples; both showed abnormal expression for PPAR- γ and SAA1, one of two for PPAR- δ and neither was abnormal for IL-8 and COX-2. Thus, for this case, 5 of 10 tested were beyond the upper

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0.01 boundary. The probability that this happened by

chance is 2.4×10^{-8} . The general formula is given by: $\Pr\{x \geq k \mid p, n\} = \sum_{i=k}^{5n} (0.01)^i (0.99)^{5n-i}$

5 where k is the number beyond the 99 percentile and n is the number of samples (5 is the number of genes tested).

Results

Altered gene expression in the rectosigmoid mucosa of individuals with a family history of colon cancer:

10 Twelve individuals (ten women and two men) comprised the group with a family history of colon cancer; 16 individuals (nine women and seven men) served as the control group. (Table 1.) We analyzed a total of 92 ascending colon biopsy samples, 85 transverse colon samples, 94 descending colon biopsy samples and 181 rectosigmoid biopsy samples for levels of expression of 16 genes. Expressions of these genes are known to be altered in
15 the late stages of human colon cancers. We have also shown that some of these genes are altered in the MNM from surgical resections of colon cancer patients.

Continuing to refer to Table 1, results represent analysis of 104 biopsy samples from the 16 individuals without family history and 77 biopsy samples from 12 individuals with family history of colon cancer in a first-degree relative. Samples were analyzed for
20 gene expression as described in Methods. The numbers in the table represent the expression level relative to the average MC_T of the control group. If there is no variation among individuals, the normal gene expression level in the control group should equal to 1. Multivariate analysis using the Wilks Lambda criterion was carried out on log2 expression values of the 16 genes to determine the significance of the difference between
25 the two groups. Genes are listed from smallest to largest P value.

Multivariate analysis of the expression values of all 16 genes indicated a significant difference in the biopsy samples from the rectosigmoid region ($p = 0.01$) between those with and those without a family history of sporadic colon cancer. Gene expression in biopsy samples from the descending, ascending and transverse colon did not vary significantly
30 between these two groups of individuals ($p = 0.06$, 0.22 and 0.52 respectively). Most of the differences in rectosigmoid biopsy samples were contributed by just five of these genes (Table 1): PPAR- γ , SAA1, IL-8, COX-2 and PPAR- δ . Similar to the alterations of gene expression in the MNM of cancer patients, we found that the expression levels of SAA1, IL-8 and COX-2 were up-regulated and those of PPAR- γ and PPAR- δ were down-regulated
35 in the MNM of individuals with a family history of sporadic colon cancer.

The mean (\pm SD) age in the family history group was younger (45 ± 12 years) than that of the control group (56 ± 16 years), presumably because of heightened awareness of the need for early colonoscopy in the group with a family history of colon cancer. In addition, there is a sex difference between these two groups (ten women and two men in the family history group versus nine women and seven men in the control group). However, we found that sex did not affect the level of gene expression ($p=0.67$). Moreover, there was no correlation between age and the expression levels of SAA1, IL-8, COX2 and PPAR- γ (all $p > 0.05$) except for PPAR- δ 0.01). Nevertheless, abnormal expression (down-regulation) of PPAR- δ increases with age. Thus comparison between younger family history group and older controls, would be biased toward finding fewer, rather than more, abnormal expressions in the family history group. In other words, we may underestimate the incidence of altered expression of PPAR- δ in the family history group.

Table 1. Gene expression levels in normal rectosigmoid biopsy samples from individuals with family history of colorectal cancer as compared with controls

Genes	Controls (n=104)		Patients with family history (n=77)		P Values
	Range	Mean \pm (S.D.)	Range	Mean \pm (S.D.)	
PPAR- γ	0.44 - 1.65	1.07 \pm 0.41	0.20 - 2.59	0.79 \pm 0.40	0.006
SAA1	0.17 - 22	2.16 \pm 3.67	0.33 - 2343	151 \pm 452	0.02
IL-8	0.14 - 13	1.71 \pm 1.94	6.84 - 13	6.84 \pm 2.82	0.02
COX-2	0.17 - 18	1.82 \pm 2.75	0.24 - 30	5.11 \pm 9.01	0.07
PPAR- δ	0.39 - 2.66	1.11 \pm 0.48	0.16 - 2.22	0.89 \pm 0.46	0.07
CD44	0.35 - 4.13	1.14 \pm 0.64	0.11 - 4.98	1.41 \pm 0.78	0.12
c-Myc	0.24 - 3.66	1.21 \pm 0.75	0.26 - 4.31	1.48 \pm 0.82	0.14
MCSF-1	0.38 - 22	1.81 \pm 2.59	0.20 - 11	2.04 \pm 2.19	0.21
Gro- α	0.01 - 51	2.61 \pm 5.48	0.34 - 57	5.76 \pm 11.63	0.22
Gro- γ	0.16 - 35	2.18 \pm 4.29	0.12 - 41	2.55 \pm 5.91	0.25
P21	0.51 - 2.15	1.10 \pm 0.62	0.20 - 7.68	0.90 \pm 0.32	0.27
PPAR- α	0.31 - 2.38	1.09 \pm 0.55	0.26 - 2.21	1.00 \pm 0.40	0.54
CXCR2	0.22 - 13	1.45 \pm 1.78	0.43 - 4.44	1.49 \pm 1.55	0.55
OPN	0.19 - 13	1.66 \pm 2.05	0.15 - 12	1.41 \pm 1.92	0.73
CyclinD	0.34 - 3.48	1.28 \pm 0.85	0.13 - 3.21	1.29 \pm 0.79	0.81
COX-1	0.27 - 5.97	1.21 \pm 0.85	0.25 - 2.63	1.09 \pm 0.51	0.87

Comparison with cut-off points for "normal" gene expression

Relative gene expression levels in the rectosigmoid samples varied among individuals, much more so in samples obtained from the individuals with a family history of

colon cancer than the corresponding values from the controls (Table 1). We therefore use the expression level of each gene in the control group to define the "normal" expression level for each gene by calculating a cut-off point ($p = 0.01$) for each gene. Figure 3 shows the distribution of the log (base2) expression values for genes, PPAR- γ , IL-8, SAA 1 and COX-2 and their cut-off points. As expected, less than 1% of the biopsy samples from the control group had expression of these genes above or below the cut-off lines ($p = 0.01$, Figure 3). However, 21%, 12% and 8% of the biopsy samples from the family history group had expression of SAA1, IL-8 and COX-2, respectively, above the cut-off points, and 12% of them had expression of PPAR- γ below the cut-off point (Table 2).

10

Table 2. Number of biopsy samples (N) with gene expression above/below the cut-off point in normal individuals and individuals with a family history of colon cancer

Genes	Biopsy samples from Normal Controls (n=104) N (%)	Biopsy samples from individuals with Family History (n= 77) N (%)
PPAR- γ	0	9 (12%)†‡
SAAI	0	16(21%)*‡
IL-8	0	9 (12%)*‡
COX-2	1 (1%)*	6 (8%)*‡
PPAR- δ	0	2 (3%)†
Gro- γ	1 (1%)*	2 (3%)*
PPAR- α	0	2 (3%)†
Gro- α	0	0
MCSF-1	1 (1%)*	0
OPN	1 (1%)*	0
P21	0	0
CD44	1 (1%)*	0
CXCR2	1 (1%)*	0
c-Myc	0	0
CyclinD	0	0
COX-1	0	0

15

† with gene expression level below the cut-off point

* with gene expression level above the cut-off point

‡ number of patients with alterations are listed in Table 3.

We next analyzed each individual in the family history group (Table 3). The number of biopsy samples which exhibited expression levels below (for PPAR- γ and δ) or above (for IL-8, SAA1 and COX-2) the cut-off point ($p=0.01$) are indicated. Individuals with all the biopsy samples exhibiting expression levels within the normal range are indicated with a (-) sign. All the grandparents with colon cancers in this study are maternal. Ages of the family member when colon cancer was diagnosed are indicated as follows: *** indicates that colon cancer was diagnosed before 50 years of age; ** indicates before 60 years of age; and * indicates after 60 years of age. Ages of the rest of the family members when colon cancer was diagnosed are not available. None of the twelve patients in the family history group reported other types of cancer in the family except that father of the patient for case #10 had lung cancer in the 1970's.

As evidenced in Table 3, for the five most commonly altered genes, nine of the twelve individuals with a family history of colon cancer had at least one biopsy sample with expression levels below or above the cut-off point. Two individuals (cases #1 and 2) had altered expression of three of these genes in apparently normal rectosigmoid mucosa. In contrast, only one of the sixteen individuals in the control group had altered expression of one of these five genes (see Table 2). The cut-off is set so that 1% of expressions could be false positives. However, the numbers of biopsy samples obtained from each individual are different. To make an adjustment for the number of specimens, we also calculated, for each case, the probability that the number of observed samples outside the upper 99 percentile was due to chance. This calculation was based on the binomial distribution. As shown in Table 3, the observed altered gene expression in seven of the twelve individuals of the family history group is unlikely due to chance ($p < 0.01$). In these seven cases, expressions of at least two of the five genes were altered. In addition, among the sixteen genes analyzed, PPAR- γ and SAA1 are the most frequently altered genes that occurred in five of the twelve individuals with a family history of colon cancer (Table 3).

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Table 3. Summary of Expression of PPAR- γ , IL-8, SAA1, COX-2 and PPAR- δ in Rectosigmoid Biopsy Samples from Individuals with a Family History of Colon Cancer

Case	Sex	Age (years)	Family member with cancer	# of biopsy samples analyzed	# of samples with altered expression					# of genes with altered expression	Probability that changes are due to chance
					PPAR- γ	SAA1	IL-8	COX-2	PPAR- δ		
1	F	53	mother***	2	2	2	-	-	1	3	<0.001
2	F	53	mother*	6	2	-	1	-	1	3	<0.001
3	M	43	father*	5	3	1	-	-	-	2	<0.001
4	F	47	mother*	7	-	7	1	-	-	2	<0.001
5	F	52	mother	8	-	-	-	-	-	0	1
6	F	52	Father and daughter***	6	-	-	1	-	-	1	0.26
7	F	18	grandfather and sister***	8	2	-	-	1	-	2	<0.01
8	F	35	Mother* and grandmother	8	-	-	8	6	-	2	<0.001
9	F	46	father**	8	-	-	-	-	-	0	1
10	F	64	sister*	6	-	1	-	-	-	1	0.26
11	F	36	mother and grandfather	7	-	-	-	-	-	0	1
12	M	38	mother and grandfather	6	1	6	-	-	-	2	<0.001

of individuals with altered gene expression

5 5 4 2 2

Expression of different genes are altered at different sites of MNCM from individuals with a family history of colon cancer.

Analysis of individual cases from the family history group showed that different genes were altered in rectosigmoid biopsy samples in different subjects. For instance, SAA1 and PPAR- γ were altered in case #3, IL-8 and SAA1 were altered in case #4; while COX-2 and IL-8 but not SAA1 were altered in case #8 (Figure 4A). In addition, some genes were altered in all the rectosigmoid biopsy samples from the same patient (such as SAA 1 in case #4 and IL-8 in case #8), while others were only altered in some of these biopsy samples (*i.e.* SAA1 and PPAR- γ in case #3, IL-8 in case #4 and COX-2 in case #8). In addition, some of these alterations are restricted to the rectosigmoid regions; such as IL-8 in case #4; while others can be extended to other regions of the colon, such as SAAI in case #4 (Figure 4B).

We also observed that the difference in gene expression between the two groups of individuals increased along the length of the colon for PPAR- γ ($p=0.001$ for trend) and SAA1 ($p < 0.001$), but not for IL-8 ($p = 0.20$), COX2 ($p = 0.58$), nor PPAR- δ ($p = 0.54$). These results suggest that there is an increasing abnormality along the colon going from the ascending to the rectal portion between the two groups of individuals that can be detected despite reduced numbers of samples toward the ascending portion in this study.

From the foregoing example, it was possible to draw the following conclusions. Approximately 5-10% of colorectal cancers occur among patients with one of the two autosomal dominant hereditary forms of colon cancer (familial adenomatous polyposis and hereditary nonpolyposis colorectal cancer), or who have inflammatory bowel disease (Burt R., Peterson G.M. In: Young G., Rozen, P. & Levin, B. Saunders, ed. in *Prevention and Early Detection of Colorectal Cancer*, Philadelphia, 171-194 (1996)). Of the remaining colon cancers, approximately 20% are associated with a family history of colon cancer, which is associated with a two-fold increased risk of developing colon cancer (Smith R.A., von Eschenbach A.C., Wender R., *et al.*, *American Cancer Society guidelines for the early detection of cancer: update of early detection guidelines for prostate, colorectal, and endometrial cancers*, and *Update 2001—testing for early lung cancer detection*, 51 CA Cancer J Clin. 38-75; quiz 77-80 (2001)). Although linkage to chromosomes 15q13-14 and 9q22.2-31.2 has been reported in a subset of patients with familial colorectal cancer (Wiesner G.L., Daley D., Lewis S., *et al.*, *A subset of familial colorectal neoplasia kindreds linked to chromosome 9q22.2-31.2*, 100 Proc Natl Acad Sci U S A, 12961-5 (2003)), the genetic basis for most of these cases is not known. In this study, we have demonstrated substantial alterations in the expression of PPAR- γ , IL-8 and SAAI in the rectosigmoid MNCM from individuals with a family history of sporadic colon cancer, even though these individuals had no detectable colon abnormalities. Our previous study showed that, in addition to PPAR- γ , IL-

8 and SAA1, expressions of PPAR- δ , p21, OPN, COX-2, CXCR2, MCSF-1 and CD44 were also altered significantly in the MNCM of colon cancer patients when compared to normal controls without colon cancer, polyps, or family history. These observations suggest that altered expression of genes related to cancer development in the MNCM may be a sequential event and may occur earlier than the appearance of gross morphological abnormalities. For example, altered expression of PPAR- γ , SAA1 and IL-8 may occur in MNCM of individuals who have not developed colon cancer, but are at high risk of doing so; while altered expressions of other genes, such as PPAR- δ , p21, OPN, COX-2, CXCR2, MCSF-1 and CD44, may occur later in MNCM of individuals who have already developed a colon cancer (Chen L-C, Hao C-Y, Chiu Y.S.Y., *et al.*, *Alteration of Gene Expression in Normal Appearing Colon Mucosa of APC^{min} Mice and Human Cancer Patients*, 64 Cancer Research 3694-3700 (2004)).

Genetic and epigenetic changes have been reported in macroscopically normal tissues for several neoplasms (Tycko B., *Genetic and epigenetic mosaicism in cancer precursor tissues*, 983 Ann N Y Acad Sci., 43-54 (2003)). For example, allelic loss has been demonstrated in normal breast terminal ductal lobular units adjacent to primary breast cancers. (Deng G., Lu Y., Zlotnikov G., Thor A.D., Smith H.S., *Loss of heterozygosity in normal tissue adjacent to breast carcinomas*, 274 Science, 2057-9 (1996)). Such allelic loss is associated with an increased risk of local recurrence (Li Z., Moore D.H., Meng Z.H., Ljung B.M., Gray J.W., Dairkee S.H., *Increased risk of local recurrence is associated with allelic loss in normal lobules of breast cancer patients*, 62 Cancer Res., 1000-3 (2002)). In addition, normal-appearing colonic mucosal cells from individuals with a prior colon cancer are more resistant to bile acid-induced apoptosis than mucosal cells from individuals with no prior colon cancer (Bernstein C., Bernstein H., Garewal H., *et al.*, *A bile acid-induced apoptosis assay for colon cancer risk and associated quality control studies*, 59 Cancer Res., 2353-7 (1999); and Bedi A., Pasricha P.J., Akhtar A.J., *et al.*, *Inhibition of apoptosis during development of colorectal cancer*, 55 Cancer Res., 1811-6 (1995)). Since apoptosis is important in colonic epithelium to eliminate cells with unrepaired DNA damage (Payne C.M., Bernstein H., Bernstein C., Garewal H., *Role of apoptosis in biology and pathology: resistance to apoptosis in colon carcinogenesis*, 19 Ultrastruct Pathol., 221-48 (1995)), reduction in apoptosis could result in the retention of DNA-damaged cells and increase the risk of carcinogenic mutations.

PPAR- γ is down-regulated in several carcinomas. Ligands of PPAR- γ inhibit cell growth and induce cell differentiation (Kitamura S., Miyazaki Y., Shinomura Y., Kondo S., Kanayama S., Matsuzawa Y., *Peroxisome proliferator-activated receptor gamma induces growth arrest and differentiation markers of human colon cancer cells*, 90 Jpn J Cancer Res 75-80 (1999)), and loss-of-function mutations in PPAR- γ have been reported in human colon cancer (Sarraf P., Mueller E., Smith W.M., *et al.*, *Loss-of-function mutations in PPAR gamma*

associated with human colon cancer, 3 Mol. Cell, 799-804 (1999)). Thus, our observation of down-regulation in PPAR- γ expression in MNCM may represent an early event that promotes colonic epithelial cell growth and inhibits cellular differentiation. In addition, PPAR- γ also negatively regulates inflammatory response (Welch J.S., Ricote M., Akiyama T.E., Gonzalez F.J., Glass C.K., *PPAR gamma and PPAR delta negatively regulate specific subsets of lipopolysaccharide and IFN-gamma target genes in macrophages*, 100 Proc Natl Acad Sci U S A 6712-7 (2003)). Inflammation favors tumorigenesis by stimulating angiogenesis and cell proliferation (Nakajima N., Kuwayama H., Ito Y., Iwasaki A., Arakawa Y., *Helicobacter pylori*, neutrophils, interleukins, and gastric epithelial proliferation, 25 Suppl. 1 J Clin Gastroenterol., 98-202 (1997)). Similarly, IL-8 and the acute-phase protein SAA1 modulate the inflammatory process (Dhawan P., Richmond A., *Role of CXCL 1 in tumorigenesis of melanoma*, 72 J Leukoc Biol., 9-18 (2002); and Urieli-Shoval S., Linke R.P., Matzner Y., *Expression and function of serum amyloid A, a major acute-phase protein, in normal and disease states*, 7 Curr Opin Hematol., 64-9 (2000)). Up-regulation of pro-inflammatory cytokines and acute phase proteins has been reported in the colon mucosa of individuals with inflammatory bowel disease (Niederau C., Backmerhoff F., Schumacher B., *Inflammatory mediators and acute phase proteins in patients with Crohn's disease and ulcerative colitis*, 44 Hepatogastroenterology, 90-107 (1997); and Keshavarzian A., Fusunyan R.D., Jacyno M., Winship D., MacDermott R.P., Sanderson I.R., *Increased interleukin-8 (IL-8) in rectal dialysate from patients with ulcerative colitis: evidence for a biological role for IL-8 in inflammation of the colon*, 94 Am J Gastroenterol., 704-12 (1999)), who are at very high risk of developing colon cancer (Bachwich D.R., Lichtenstein G.R., Traber P.G., *Cancer in inflammatory bowel disease*, 78 Med Clin North Am., 1399-412 (1994)). Epidemiological observations also suggest that chronic inflammation predisposes to colorectal cancer (Rhodes J.M., Campbell B.J., *Inflammation and colorectal cancer: IBD-associated and sporadic cancer compared*, 8 Trends Mol Med., 10-6 (2002); and Farrell R.J., Peppercorn M.A., *Ulcerative colitis*, 359 Lancet 331-40 (2002)). Thus, the observation of down-regulation of PPAR- γ and up-regulation of IL-8 and SAA1 in the normal mucosa of individuals with a family history of sporadic colon cancer and individuals with inflammatory bowel disease may indicate the involvement of common pathways leading to colon carcinogenesis in these two groups.

Our observation of altered expression of genes associated with cancer and inflammation in normal colonic mucosa in some individuals with a family history of colon cancer is consistent with the recent report of association of elevated serum C-reactive protein ("CRP") concentration prior to the development of colon cancer (Erlinger T.P., Platz E.A., Rifai N., Helzlsouer K.J., *C-reactive protein and the risk of incident colorectal cancer*, 291 JAMA, 585-90 (2004)). These findings suggest that inflammation is a risk factor for the development

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of colon cancer in average-risk individuals (*id.*). However, CRP is a nonspecific marker of inflammation that may indicate inflammation in tissues other than colon. In our study, we have analyzed the tissue where colon cancer arises and would be more specific in assessing the risk of developing colon cancer.

5 We do not know which cell type is responsible for the observed altered gene expression. There are many cell types in the colonic mucosa, including several types of mucosal epithelial cells, stromal cells and blood-born cells. Studies from our group and others have demonstrated that the up-regulation of COX-2 protein in MNCM is localized primarily to the infiltrating macrophages and secondarily to the epithelial cells in aberrant crypt
10 foci in the MNCM of APC^{min} mice (Chen L-C, Hao C-Y, Chiu Y.S.Y., *et al.*, *Alteration of Gene Expression in Normal Appearing Colon Mucosa of APC^{min} Mice and Human Cancer Patients*, 64 Cancer Research 3694-3700 (2004); and Hull M.A., Booth J.K., Tisbury A., *et al.*, *Cyclooxygenase 2 is up-regulated and localized to macrophages in the intestine of Min mice*, 79 Br J Cancer, 1399-405 (1999)). From our previous studies of MNCM of APC^{min} mice,
15 detection of the gene products that are up- or down- regulated in MNCM by immunohistochemical staining was found to be technically difficult, perhaps because the secreted proteins, such as IL-8 and SAA1, are evanescent in tissue sections (Chen L-C, Hao C-Y, Chiu Y.S.Y., *et al.*, *Alteration of Gene Expression in Normal Appearing Colon Mucosa of APC^{min} Mice and Human Cancer Patients*, 64 Cancer Research 3694-3700 (2004)). Due to
20 the limited amount of the biopsy samples and technical difficulties, we were unable to perform immunohistochemical staining to demonstrate the cell types contributing to the altered gene expression. If the absolute RNA quantities are sufficient, RNA *in situ* hybridization may be a better method to determine the cellular locations of alterations. Alternatively, laser microdissection followed by RT-PCR may be able to define the cell types involved.
25 Regardless of the cell types responsible for the altered gene expression, our results demonstrate that relative to normal individuals without family history of colon cancer, altered gene expression is present in normal colon mucosa of some individuals with a family history of colon cancer and these individuals are known to have an increased risk of developing colon cancer (Burt R., Peterson G.M. In: Young G., Rozen, P. & Levin, B. Saunders, ed. in
30 *Prevention and Early Detection of Colorectal Cancer*, Philadelphia, 171-194 (1996)).

Among patients with altered gene expression in the rectosigmoid biopsy samples, some showed alterations in all biopsy samples (*i.e.*, expression of SAA1 in cases #4 and 12), while others showed altered expression in some biopsy samples only (*i.e.*, PPAR- γ in cases #2 and #3, figure 2). Since most samples were assayed with multiple genes in duplications to
35 ensure the quality of cDNA, such heterogeneity is unlikely due to technical variation. We speculate that this heterogeneity might reflect the frequency and/or the distribution of "hot

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spots" in these individuals. It is possible that the individuals with altered gene expression in all rectosigmoid biopsy samples may have wide-spread molecular abnormalities in their rectosigmoid mucosa, while those with altered expression in some of the biopsy samples have discrete hot spots. Thus, individuals in the former group may have a global predisposition to development of colon polyps or cancer, while those in the latter group may have local predisposition. Whether the risks in developing colon cancer or polyps differ between these two groups is unknown. In addition, altered expression of different combination of genes were observed in the rectosigmoid biopsy samples of individuals in the family history group. This observation suggests that different molecular pathways may be involved in the early stages of colon carcinogenesis. Whether altered gene expression in certain molecular pathways is associated with higher risk of polyps or cancer also remains to be determined.

Consistent with the reports of more aberrant crypt foci (the preneoplastic colonic lesions) in the distal colon than in the proximal colon of the sporadic colon cancer patients and the carcinogen-treated mice (Shpitz B., Bomstein Y., Mekori Y., *et al.*, *Aberrant crypt foci in human colons: distribution and histomorphologic characteristics*, 29 Hum Pathol., 469-75 (1998); and Salim E.I., Wanibuchi H., Morimura K., *et al.*, *Induction of tumors in the colon and liver of the immunodeficient (SCID) mouse by 2-amino-3-methylimidazo[4,5-f]quinoline (IQ)-modulation by long chain fatty acids*, 23 Carcinogenesis, 1519-29 (2002)), we found that most of the alterations in gene expression were found in the distal colon of the individuals from the family history group. We speculate that the distal colon mucosa of the susceptible individuals may be exposed to higher concentration of exogenous substances present in the stool than mucosa in other colon regions after most of the water is re-absorbed at the end of the large intestine, and such exposure may lead to higher rate of altered gene expression at this region.

We have shown that family history of colon cancer, but not age or sex, is the factor responsible for the observed differences in gene expression in the rectosigmoid mucosa of the two groups. The available information did not indicate any specific difference in diet or medication between these two groups of patients. However, we cannot eliminate the possibility that diet or medication affect gene expression without further study. Not all individuals with a family history of colon cancer will develop cancer or adenomatous polyps of the colon (Smith, R.A., von Eschenbach A.C., Wender, R., *et al.*, *American Cancer Society guidelines for the early detection of cancer: update of early detection guidelines for prostate, colorectal, and endometrial cancers, and Update 2001—testing for early lung cancer detection*, 51 CA Cancer J. Clin., 38-75; quiz 77-80 (2001).). Consistent with this clinical observation, our analysis also showed that not all the individuals with a family history of colon

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cancer have altered gene expression in MNCM. Since the genes analyzed in this study are involved in the development of colon cancer, we hypothesize that individuals with altered gene expression in the MNCM may be more susceptible to developing polyps or cancer than those without altered gene expression. To test this hypothesis, a prospective study with a larger number of study subjects will be needed. If such an association is confirmed, it may be possible to identify individuals at increased risk of developing colon cancer by using gene expression analysis of rectosigmoid biopsy samples. Theoretically, it is easier to identify individuals with global alterations in the MNCM than individuals with local alterations by analysis of random MNCM samples. However, if an appropriate panel of genes was selected for analysis using multiple samples, it may have enough predictive power to identify such patients.

Turning now to **Fig. 5**, various aspects of **Fig. 5** may be implemented using a conventional general purpose or specialized digital computer(s) and/or processor(s) programmed according to the teachings of the present disclosure, as will be apparent to those skilled in the computer arts. Appropriate software coding can be prepared readily by skilled programmers based on the teachings of the present disclosure, as will be apparent to those skilled in the software arts. The invention also may be implemented by the preparation of integrated circuits and/or by interconnecting an appropriate network of component circuits, as will be readily apparent to those skilled in the arts.

Various aspects include a computer program product which is a storage medium having instructions and/or information stored thereon/in which can be used to program a general purpose or specialized computing processor(s)/device(s) to perform any of the features presented herein. The storage medium can include, but is not limited to, one or more of the following: any type of physical media including floppy disks, optical discs, DVDs, CD-ROMs, microdrives, magneto-optical disks, holographic storage devices, ROMs, RAMs, EPROMs, EEPROMs, DRAMs, PRAMS, VRAMs, flash memory devices, magnetic or optical cards, nano-systems (including molecular memory ICs); paper or paper-based media; and any type of media or device suitable for storing instructions and/or information. Various aspects include a computer program product that can be transmitted in whole or in parts and over one or more public and/or private networks wherein the transmission includes instructions and/or information which can be used by one or more processors to perform any of the features presented herein. In various aspects, the transmission may include a plurality of separate transmissions.

Stored on one or more of the computer readable medium (media), the present disclosure includes software for controlling both the hardware of general purpose/specialized computer(s) and/or processor(s), and for enabling the computer(s) and/or processor(s) to

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interact with a human user or other mechanism utilizing the results of the present invention. Such software may include, but is not limited to, device drivers, operating systems, execution environments/containers, user interfaces and applications.

5 The execution of code can be direct or indirect. The code can include compiled, interpreted and other types of languages. Unless otherwise limited by claim language, the execution and/or transmission of code and/or code segments for a function can include invocations or calls to other software or devices, local or remote, to do the function. The invocations or calls can include invocations or calls to library modules, device drivers and remote software to do the function. The invocations or calls can include invocations or calls in
10 distributed and client/server systems.

Fig. 6 depicts an aspect of this disclosure having a swab sampling and transport system **400** for the minimally invasive sampling of colonic mucosal cells. The system **400** of **Fig. 6** is comprised of a swab **410** and a container **420**. A container **420**, such as one depicted by the aspect of the disclosure shown in **Fig. 6**, is configured to stabilize, extract,
15 and store the sample of colonic mucosal cells until the diagnostic test for early detection of CRC using the disclosed biomarker panel can be done on the sample.

The swab **410** has a tip **412** extending from the end of a shaft **414**. The tip **410** may be of a number of shapes such as oblate, square, rectangular, round, etc., and has a maximum width of about 0.5 cm to 1.0 cm, and a length of about 1.0 cm to 10.0 cm around
20 the end of the rod. The tip **412** may be composed of a number of materials, such as cotton, rayon, polyester, and polymer foam, for example, or combinations of such materials. The shaft **414** is made of a material with sufficient mechanical strength for effectively swabbing the rectal area, but with enough flexibility to prevent injury. Examples of shaft materials having the strength and flexibility properties for a rectal swab include wood, paper, and a variety of
25 polymeric materials, such as polyester, polystyrene, and polyurethane, and composites of such polymers.

The container **420** has a body **412** and a cap **424**. The body **412** may have a variety of lengths and diameters to accommodate a swab **410** having dimensions of the tip **412** and the range of lengths of the shaft **414** as described in the above. The body **412** of the
30 container may be made of a number of polymeric materials, such as polyethylene, polypropylene, polycarbonate, polyfluorocarbon, or glass, while the cap **424** typically is made of a desirable polymeric material, such as the examples given for the body **412**. The container **420** has a reagent **426** in the bottom that is suitable for stabilizing and extracting the colonic mucosal cells collected on the swab **410** when swabbing of the rectal area is done as
35 a minimally invasive sampling technique. Additionally, a container **420** having a reagent **426**

suitable for stabilizing and extracting a sample of colonic mucosal cells from a stool sample may be used without the need for the swab **410**.

The reagent **426** contains a buffered solution of guanidine thiocyanate in a concentration of at least about 0.4M and other tissue denaturing reagents such as a biological surfactant in a concentration of at about between 0.1 to 10%. Desirable biological surfactants can be zwitterionic, such as CHAPS or CHAPSO, non-ionic, such as TWEEN, or any of the alkylglucoside surfactants, or ionic, such as SDS. A variety of buffers, for example, those generally known as Good's buffers, such as Tris, may be used. The concentration of the buffer may vary in order to buffer the reagent **426** effectively to a pH of between about 7.0 to 8.5.

It is further contemplated that the sample taken using an aspect of the disclosure as in **Fig. 6** of a swab sampling and transport system **400** can be processed and the data analyzed in a single apparatus using the computer hardware and software disclosed above. That is, the sample obtained from the aspect of the disclosure of **Fig. 6** can be analyzed according to **Fig. 5** in a single apparatus. However, it is also contemplated that a patient's blood or stool sample can be analyzed in the single apparatus. In one embodiment, one aspect of the apparatus is a first component that is used to carry out RT-PCR for a sample from a patient for gene expression profiling, as described above. Gene expression profiling allows quantifying of cDNA of SEQ. ID Nos 1-16, which is reverse-transcribed from mRNA made by cells in the sample from the patient. The sets of primers from SEQ. ID Nos 33-64 are used in the RT-PCR reaction to prime strands of mRNA corresponding to SEQ. ID Nos 1-16, and thereby to synthesize cDNA corresponding to SEQ. ID Nos 1-16.

After obtaining the cDNAs from the RT-PCR, data are compared by a second component of the apparatus to control data already stored in the apparatus on a storage medium. Multivariate analysis as disclosed above is applied using software to execute instructions for the ANOVA, M-Dist, or other means of multivariate analysis. Based on the statistical analysis, a qualified diagnostician can assess the presence or absence of CRC, the progress of CRC, and/or the effects of treatment of CRC.

In a further aspect of this disclosure, protein expression profiling of patient samples can be carried out for early detection of CRC, using a single apparatus. The term "polypeptide" or "polypeptides" is used interchangeably herein with the term "protein" or "proteins." As discussed previously, proteins long have been investigated for their potential as biomarkers, with limited success. There is value in protein biomarkers as complementary to polynucleotide biomarkers. Reasons for having the information provided by both types of biomarkers include the current observations that mRNA expression levels are not good predictors of protein expression levels, and that mRNA expression levels tell nothing of the

post-translational modifications of proteins that are key to their biological activity. Therefore, in order to understand the expression levels of proteins, and their complete structure, the direct analysis of proteins is desirable.

Disclosed herein are proteins listed in SEQ. ID NOs 17-32, which correspond to the
5 genes indicated in SEQ. ID NOs 1-16. A further aspect of the disclosed invention is to determine expression levels of the proteins indicated by SEQ. ID NOs. 17-32. A sample from the patient, taken by non- or minimally-invasive methods as disclosed above, can be used to prepare fixed cells or a protein extract of cells from the sample. The cells for protein expression profiling can be obtained either through the method of **Fig. 6**, or alternatively for
10 example by a blood sample or stool sample, or other non-invasive or minimally invasive method (or of course by more conventional invasive methods, including for example sigmoidoscopy and other procedures).

In a first component of the apparatus, the cells or protein extract can be assayed with a panel of antibodies – either monoclonal or polyclonal – against the claimed panel of
15 biomarkers for measuring targeted polypeptide levels. The objective of the assay is to detect and quantify expression of proteins corresponding to the biomarker gene sequences in SEQ. ID NOs 1-16, *i.e.*, SEQ. ID NOs 17-32.

In one aspect of the disclosure contemplated for the method, the antibodies in the antibody panel, which are based on the panel of biomarkers, can be bound to a solid support.
20 The method for protein expression profiling may use a second antibody having specificity to some portion of the bound, targeted polypeptide. Such second antibody may be labeled with molecules useful for detecting and quantifying the bound polypeptides, and therefore in binding to the polypeptide, label it for detection and quantification. Additionally, other reagents are contemplated for labeling the bound polypeptides for detection and
25 quantification. Such reagents may either directly label the bound polypeptide or, analogous to a second antibody, may be a moiety with specificity for the bound polypeptide having labels. Examples of such moieties include but are not limited to small molecules such as cofactors, substrates, complexing agents, and the like, or large molecules such as lectins, peptides, oligonucleotides, and the like. Such moieties may be either naturally occurring or synthetic.

30 Examples of detection modes contemplated for the disclosed methods include, but are not limited to spectroscopic techniques, such as fluorescence and UV-Vis spectroscopy, scintillation counting, and mass spectroscopy. Complementary to these modes of detection, examples of labels for the purpose of detection and quantitation used in these methods include, but are not limited to chromophoric labels, scintillation labels, and mass labels. The
35 expression levels of polynucleotides and polypeptides measured in a second component of the apparatus using these methods may be normalized to a control established for the

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purpose of the targeted determination. The control data is stored in a computer which is a third component of the apparatus.

A fourth software component compares the data obtained from a patient's or a plurality of patients' samples to the control data. The comparison will comprise at least one
5 multivariate analysis, and can include ANOVA, MANOVA, M-Dist, and others known to those of ordinary skill in the art. Once the statistical analysis and comparison is performed and complete, a physician or other qualified person can make a diagnosis concerning the patient's or patients' CRC status.

Turning now to the drug screening aspect of the present disclosure, it is noted that the
10 panel of biomarkers disclosed herein are genes and expression products thereof that also are known to be involved in the following metabolic pathways and processes: 1) oxidative stress/inflammation; 2) APC/b-catenin pathway; 3) cell cycle/ transcription factors; and 4) actions of cytokines and other factors involved in cell/cell communications, growth, repair and response to injury or trauma. There is increasing evidence that these pathways, and hence
15 members of the subject panel of biomarkers, are also involved in many other kinds of cancers than CRC, such as lung, prostate and breast, as well as neurodegenerative diseases, such as Alzheimer's and amyotrophic lateral sclerosis ("ALS"). In such pathologies, genes and expression products thereof involved in these pathways are fundamental to the growth, maintenance and response to stress of cells of many different types. During a pathology such
20 as cancer or neurodegeneration, altered expression of certain altered genes results in a pathological symptom or symptoms, so that a shift in those genes, and expression products thereof, are characteristic biomarkers of that particular pathology. In that regard, seemingly unrelated pathologies, such as various cancers and neurodegenerative diseases, are manifestations of very complex pathologies that each involve discrete members of the subject
25 biomarkers, which are genes and expression products thereof drawn from the above group of pathway and processes. As practical evidence of this, it is now appreciated that COX-2 inhibitors have therapeutic value for a wide variety of disorders, including not only colon and other cancers, but for some neurodegenerative diseases as well.

What is disclosed herein is the use of the subject biomarker panel in **Fig. 1** in the drug
30 discovery process for pathologies such as cancers, for example CRC, lung prostate, and breast, and neurodegenerative diseases, for example Alzheimer's and ALS. As mentioned in the above, the discrete pattern of altered genes and expression products thereof provides a unique signature for each specific disease, so the panel provides the necessary selectivity for a variety of pathologies. What is meant by drug is any therapeutic agent that is useful in the
35 treatment of a pathology. This includes traditional synthetic molecules, natural products,

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natural products that are synthetically modified, and biopharmaceutical products, such as polypeptides and polynucleotides, and combinations, extracts and preparations thereof.

Drug screening is part of the first stage of drug development referred to as the drug discovery phase. Prospective drugs that are qualified through the drug screening process are typically referred to as leads, which is to say that in passing the criteria of the screening process they are advanced to further testing in a stage of drug discovery generally referred to as lead optimization. If passing the lead optimization stage of drug discovery, the leads are qualified as candidates, and are advanced beyond the drug discovery stage to the next stage of drug development known as preclinical trials, and are referred to as investigative new drugs ("IND"). If the IND is advanced, it is advanced to clinical trials, where it is tested in human subjects. Finally, if the IND shows promise through the clinical trial stage, after approval from FDA, it may be commercialized. The entire drug development process for a single candidate is known to take 10-15 years and hundreds of millions of dollars in development costs. For that reason, the current strategy within the pharmaceutical drug development community is to focus on the drug discovery stage as effective in weeding out prospective drugs efficiently, and advancing only candidates with high potential for success through the remaining drug development cycle.

In the screening stage of drug discovery, a specific assay for evaluating prospective drugs is performed against a qualified biological model system for which a specific endpoint is monitored. A biomarker panel that is used as a surrogate endpoint for drug screening for pathologies, such as cancers, for example CRC, lung, prostate, and breast, and neurodegenerative diseases, for example Alzheimer's and ALS, is not only a panel useful for early detection of such pathologies, but additionally demonstrates modulation by a drug in a fashion that correlates with a decrease in the pathology occurrence or recurrence. Additionally, one or more members of a biomarker panel useful in the early detection of such pathologies may also be useful as targets for drug screening for such pathologies. As will be discussed subsequently, the biomarkers described by **Fig. 1** may be useful both as surrogate endpoints in model biological systems, as well as targets in drug screening.

During the screening phase, large libraries of prospective drugs may be evaluated, representing a throughput of tens of thousands of compounds over a single screening regimen. What is regarded as low-throughput screening ("LTS") is about 10,000 to about 50,000 prospective drugs, while medium-throughput screening ("MTS") represents about 50,00 to about 100,00 prospective drugs, and high-throughput screening ("HTS") is 100,000 to about 500,000 prospective drugs.

What is meant by screening regimen includes both the testing protocol and analytical methodology by which the screening is conducted. The screening regimen, then, includes

factors such as the type of biological model that will be used in the test; the conditions under which the testing will be conducted; the type of prospective drug candidates, or library of prospective candidates that will be used; the type of equipment that will be used; and the manner in which the data are collected, processed, and stored. The scale of the screening regimen --LTS, MTS, or HIS -- is impacted by factors such as testing protocol (e.g., type of assay), analytical methodology (e.g., miniaturization, automation), and computational capability and capacity. What is meant by biological model system includes whole organism, whole cell, cell lysate, and molecular target. What is meant by prospective drug candidate is any type of molecule, or preparation or suspension of molecules, under consideration for having therapeutic use. For example, the prospective drug candidates could be synthetic molecules, natural products, natural products that are synthetically modified, and biopharmaceutical products, such as polypeptides and polynucleotides, and combinations, extracts, and preparations thereof.

As discussed above, **Fig. 1** provides sequence listings of a panel of biomarkers useful in practicing the disclosed invention. One aspect of the disclosure is a biomarker panel of 16 identified coding sequences given in SEQ. ID NOs 1-16, while another aspect of a biomarker panel is the 16 identified proteins given by SEQ. ID NOs 17-31. These two aspects of the present invention provide the selectivity and sensitivity necessary for the early detection of pathologies, such as cancers, for example CRC, lung, prostate, and breast, and neurodegenerative diseases, for example Alzheimer's and ALS.

As previously mentioned, CRC is an exemplary pathology contemplated for development of novel drugs. For CRC, no biomarker or biomarker panel has been identified that has an acceptably high degree of selectivity and sensitivity to be effective for early detection of CRC. Therefore, what is described in **Fig. 1** are aspects of biomarker panels that are differentiating in providing the basis for early detection of CRC. Selectivity of a biomarker defined clinically refers to percentage of patients correctly diagnosed. Sensitivity of a biomarker in a clinical context is defined as the probability that the disease is detected at a curable stage. Ideally, biomarkers would have 100% clinical selectivity and 100% clinical sensitivity. To date, no biomarker or biomarker panel has been identified that has an acceptably high degree of selectivity and sensitivity required to be effective for the broad range of needs in patient care management.

The analytical methodology by which the screening is conducted may include the methodologies disclosed above for early detection of CRC, *i.e.* gene expression profiling from the mRNA of a biological sample to determine the gene expression of biomarkers and how their expression level(s) might have been affected by a prospective drug candidate (including use of RT-PCR), and/or determining protein expression levels of the **Fig. 1** polypeptide

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biomarkers due to application of a prospective drug candidate; and then applying multivariate statistical analysis to determine the statistical significance of the expression levels of the various markers in the panel, with and without the prospective drug candidate(s).

Referring to **Fig. 7**, one aspect of the drug screening disclosure contemplates obtaining a tissue sample, such as a swab (see **Fig. 6**), blood sample, or biopsy, which can be taken by, for example, minimally invasive, invasive, or non-invasive means. An appropriate lysis buffer can be used to extract and preserve the RNA of the cells in the tissue sample. RT-PCR then can be carried out on the extracted RNA and converted to cDNA, as disclosed above, using, for example, at least two of the primers listed in SEQ. ID NOs 33-64, specific to the biomarker panel of **Fig. 1**, to screen the effect of the drug. The results of the assay can then be subjected to a multivariate analysis and M-dist, as disclosed above, and the results compared to control data.

Figure 8 depicts a further aspect of the drug screening disclosure in which antibodies are made against at least two biomarker proteins listed as SEQ. ID NOs 17-32, and the antibodies are used to assay a biological system, for example whole cells, cell lysates, etc. from, for example, biopsies or other tissue samples as set forth above. The antibodies are used to detect and quantify expression of the biomarker peptides identified by SEQ. ID NOs 17-32, so that the expression of these biomarker peptides can be monitored as a function of dosing the biological system with a potential drug. The results can be subjected to multivariate or univariate analysis and M-dist., as disclosed above, and compared to control data.

What has been disclosed herein has been provided for the purposes of illustration and description. It is not intended to be exhaustive or to limit what is disclosed to the precise forms described. Many modifications and variations will be apparent to the practitioner skilled in the art. What is disclosed was chosen and described in order to best explain the principles and practical application of the disclosed embodiments of the art described, thereby enabling others skilled in the art to understand the various embodiments and various modifications that are suited to the particular use contemplated.

The references cited above are incorporated by reference in full.

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CLAIMS

What is claimed:

- 5 1. A method for making a reagent composition for the early detection of colorectal cancer, lung cancer, prostate cancer, breast cancer, Alzheimer's and ALS, the method comprising:

 synthesizing a pair of primers for each polynucleotide pair from SEQ. ID NOs 33-64;
10 adjusting to at least one desired concentration in a plurality of separate stock solutions each of said primers, using a diluent;

 aliquoting each of said stock solutions of each of said primers into a plurality of
15 containers; and

 storing the plurality of containers in long-term storage conditions.
- 20 2. The method of claim 1 wherein the method further comprises lyophilizing the aliquoted stock solutions of each of said primer pairs.
- 25 3. A method for early detection of colorectal cancer, lung cancer, prostate cancer, breast cancer, Alzheimer's and ALS, the method comprising:

 obtaining a tissue sample by a non-invasive or a minimally invasive method from
 grossly-normal appearing tissue;

 isolating RNA from the sample;

30 amplifying copies of cDNA from the RNA sample using a plurality of pairs of primers selected from the group consisting of SEQ. ID NOs 33-64, to detect a panel of polynucleotides selected from SEQ. ID NOs. 1-16;

 quantifying the amplified copies of cDNA; and
35

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using the quantified amplified copies of cDNA to assess at least one of disease progress and treatment effectiveness for at least one of colorectal cancer, lung cancer, prostate cancer, breast cancer, Alzheimer's and ALS.

- 5 4. The method as in claim 3 wherein the obtaining step further comprises sampling rectal mucosal cells.
5. The method of claim 3 wherein the obtaining step further comprises one of drawing blood, sampling stool, and taking a rectal biopsy.
- 10 6. The method of claim 3 wherein the using step further comprises:
- analyzing by multivariate analysis the quantified levels of tissue sample cDNA;
- 15 comparing the multivariate analysis of the quantified levels of tissue sample cDNA with a plurality of control data, wherein the comparison determines a significance of differences from the control data to assess the presence of colorectal cancer.
- 20 7. The method of claim 6 wherein the analyzing step further comprises using one of an ANOVA test and a Mahalanobis distance test.
8. A method for early detection of colorectal cancer and for evaluation of treatment efficacy of colorectal cancer, the method comprising the steps of:
- 25 obtaining by a non-invasive or minimally-invasive method a tissue sample containing cells that grossly appear cancer-free;
- generating a plurality of antibodies having different specificities against each of the polypeptides identified by SEQ. ID NOs 17-32;
- 30 assaying for expression of polypeptides in a panel of polypeptides identified by SEQ. ID NOs 17-32 with the plurality of antibodies, wherein the assaying step allows for quantifying specific binding of the antibodies to the polypeptides;
- 35 quantifying the levels of each of the different polypeptides in the panel of polypeptides based on the quantified specific antibody binding; and

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analyzing the quantified levels of each of the different polypeptides in the panel of polypeptides, wherein the quantified levels are used to assess at least one of the presence, progress, and treatment of colorectal cancer.

5

9. The method of claim 8 wherein the obtaining step further comprises one of sampling blood, sampling stool, swabbing for colonic cells, and performing a rectal biopsy.

10

10. A method for analyzing data for the early detection and treatment monitoring of colorectal cancer, the method comprising the following steps:

obtaining a plurality of quantified levels of cDNA for polynucleotides selected from SEQ. ID Nos. 1-16 from a patient sample, wherein the sample is taken by a non-invasive method or a minimally-invasive method;

15

comparing said data from the patient sample to a plurality of stored control data using multivariate statistical analysis; and

20

making a determination concerning one of diagnosis of colorectal cancer, colorectal cancer progress, and treatment efficacy for the patient based on the comparison.

11. A machine readable medium having instructions stored thereon that, when executed by one or more processors, cause a system to:

25

obtain the data of quantified levels of cDNA for polynucleotides listed in SEQ. ID NOs. 1-16, wherein the quantified levels of cDNA are from a patient tissue sample and a control tissue sample;

30

compare the quantified levels of cDNA from the patient tissue sample to the quantified levels of cDNA from the control tissue sample using at least one multivariate statistical analysis; and

provide said multivariate statistical analysis for evaluation by an individual trained to evaluate colorectal cancer.

35

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12. A computer signal embodied in a transmission medium, comprising:

5 a code segment including instruction for obtaining quantified levels of cDNA for polynucleotides selected from SEQ. ID NOs. 1-16, wherein the quantified levels of cDNA are from a patient tissue sample;

10 a code segment including instruction for comparing the quantified levels of cDNA from the patient tissue sample to a plurality of control data using multivariate statistical analysis; and

a code segment including instruction for making a diagnosis of colorectal cancer for the patient tissue sample based on the comparison.

13. A computer signal embodied in a transmission medium, comprising:

15 a code segment including instruction for obtaining quantified levels of polypeptides selected from SEQ. ID NOs. 17-33, wherein the quantified levels of polypeptides are from a patient sample containing colonic mucosal cells;

20 a code segment including instruction for comparing the quantified levels of polypeptides from the patient sample to a plurality of control data using multivariate statistical analysis; and

25 a code segment including at least one instruction based on the comparison for at least one of a diagnosis of colorectal cancer, a progress of colorectal cancer, and an efficacy of treatment of colorectal cancer.

14. A kit for use in the early detection of colorectal cancer, the kit comprising:

30 a collection container for receiving a sample containing rectal mucosal cells obtained through a non-invasive procedure, wherein the collection container is configured to stabilize and store the sample; and

35 at least one reagent that is used in the analysis of polynucleotide expression levels, wherein the polynucleotides are selected from SEQ. ID Nos. 1-16.

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15. A kit for use in the detection of colorectal cancer, the kit comprising:

a swab sampling and sample transport system for the minimally invasive sampling of rectal mucosal cells, which system is comprised of:

5

a swab configured to sample colonic mucosal cells from the rectum; and

a collection container for receiving the swab after the sample has been taken, wherein the collection container is configured to stabilize, extract and store the sample; and

10

at least one reagent that is used in the analysis of polynucleotide expression levels, wherein the polynucleotides are selected from SEQ. ID Nos. 1-16.

15

16. A method for drug screening, the method comprising the following steps:

selecting a model biological system for at least one of colorectal cancer, lung cancer, prostate cancer, breast cancers, Alzheimer's and ALS;

20

selecting at least one prospective drug for screening using the suitable model biological system;

selecting at least two biomarkers from a panel of biomarkers identified by SEQ. ID 1-32;

25

dosing the model biological system with the at least one prospective drug; and

monitoring the response of the at least two biomarkers in the model biological system as a function of the dosing step.

30

17. The method of claim 16, further comprising: determining the efficacy of the prospective drug based on the monitoring step.

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Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
1. Coding sequence	XM_031289	Interleukin 8	IL8
2. Coding sequence	XM_051900	Prostaglandin-endoperoxide synthase 2	PTGS2
3. Coding sequence	M94582	Interleukin 8 receptor B	ILR8RB
4. Coding sequence	NM_000757	Macrophage colony stimulating factor 1	CSF1 (MCSF1)
5. Coding sequence	X54489	Melanoma growth stimulatory activity	MGSA
6. Coding sequence	NM_002090	Chemokine (C-X-C motif) ligand 3	CXCL3
7. Coding sequence	XM_032429	Secreted phosphoprotein 1	SPP1 (OPN)
8. Coding sequence	M64349	Cyclin D	CCND1
9. Coding sequence	AX057136	c-Myc	c-Myc
10. Coding sequence	L25610	Cyclin-dependent kinase inhibitor	HUMCDK1
11. Coding sequence	NM_005036	Peroxisome proliferative activated receptor, alpha	PPARA
12. Coding sequence	XM_003059	Peroxisome proliferative activated receptor, gamma	PPARG
13. Coding sequence	NM_006238	Peroxisome proliferative activated receptor, delta	PPARD
14. Coding sequence	XM_030326	CD44 antigen	CD44
15. Coding sequence	XM_044882	Prostaglandin-endoperoxide synthase 1	PTGS1
16. Coding sequence	NM_000331	Serum amyloid A1	SAA1
17. Protein	XP_031289	Interleukin 8	IL8
18. Protein	XP_051900	Prostaglandin-endoperoxide synthase 2	COX2
19. Protein	AAA36108	Interleukin 8 receptor B	CXCR2
20. Protein	NP_000757	Macrophage colony stimulating factor 1	MCSF1
21. Protein	CAA38361	Melanoma growth stimulatory activity	Groα
22. Protein	NM-002090	Chemokine (C-X-C motif) ligand 3	Groγ
23. Protein	XP_032429	Osteopontin	OPN
24. Protein	AAA52136	Cyclin D	cyclin D1
25. Protein	CAC22425	c-Myc	c-Myc

FIG. 1

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Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
26. Protein	AAA16109	Cyclin-dependent kinase inhibitor	p21
27. Protein	NP_005027	Peroxisome proliferative activated receptor, alpha	PPAR α
28. Protein	XP_003059	Peroxisome proliferative activated receptor, gamma	PPAR γ
29. Protein	NP_006229	Peroxisome proliferative activated receptor, delta	PPAR δ
30. Protein	XP_030326	CD44 antigen	CD44
31. Protein	XP_044882	Prostaglandin-endoperoxide synthase 1	COX1
32. Protein	NP_000331	Serum amyloid A1	SAA1
33. Forward primer		Interleukin 8	IL8
34. Reverse primer			
35. Forward primer		Prostaglandin-endoperoxide synthase 2	PTGS2
36. Reverse primer			
37. Forward primer		Interleukin 8 receptor B	ILR8RB
38. Reverse primer			
39. Forward primer		Macrophage colony stimulating factor 1	CSF1 (MCSF1)
40. Reverse primer			
41. Forward primer		Melanoma growth stimulatory activity	MGSA
42. Reverse primer			
43. Forward primer		Chemokine (C-X-C motif) ligand 3	MGSA
44. Reverse primer			
45. Forward primer		Secreted phosphoprotein 1	SPP1 (OPN)
46. Reverse primer			
47. Forward primer		Cyclin D	CCND1
48. Reverse primer			
49. Forward primer		c-Myc	c-Myc
50. Reverse primer			

FIG. 1 (cont'd)

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Sequence ID No. / ID	NCBI Entrez Database	Name	Abbreviation
51. Forward primer		Cyclin-dependent kinase inhibitor	HUMCDK1
52. Reverse primer			
53. Forward primer		Peroxisome proliferative activated receptor, alpha	PPAR α
54. Reverse primer			
55. Forward primer		Peroxisome proliferative activated receptor, gamma	PPAR γ
56. Reverse primer			
57. Forward primer		Peroxisome proliferative activated receptor, delta	PPAR δ
58. Reverse primer			
59. Forward primer		CD44 antigen	CD44
60. Reverse primer			
61. Forward primer		Prostaglandin-endoperoxide synthase 1	COX1
62. Reverse primer			
63. Forward primer		Serum amyloid A1	SAA1
64. Reverse primer			

FIG. 1 (cont'd)

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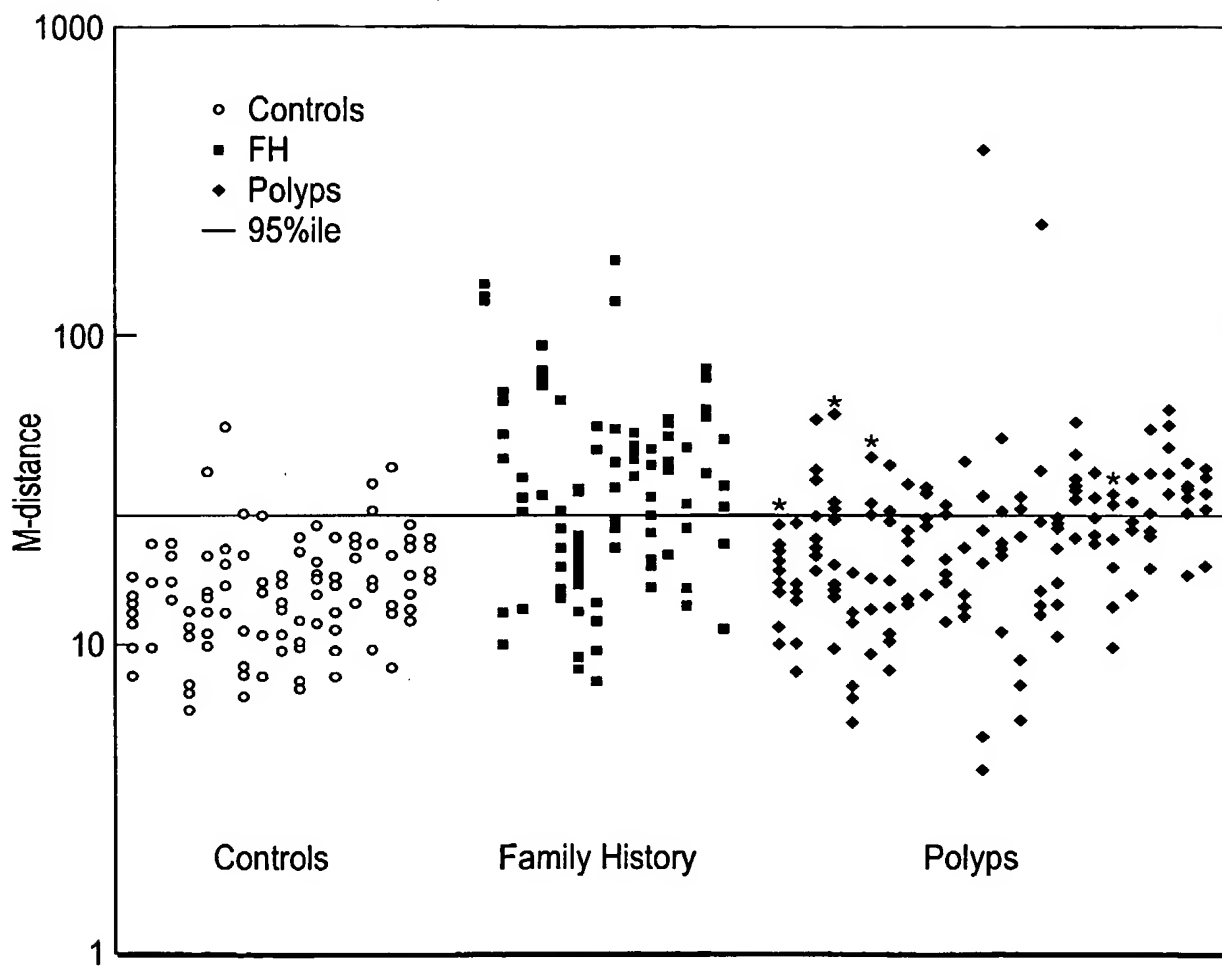


FIG. 2

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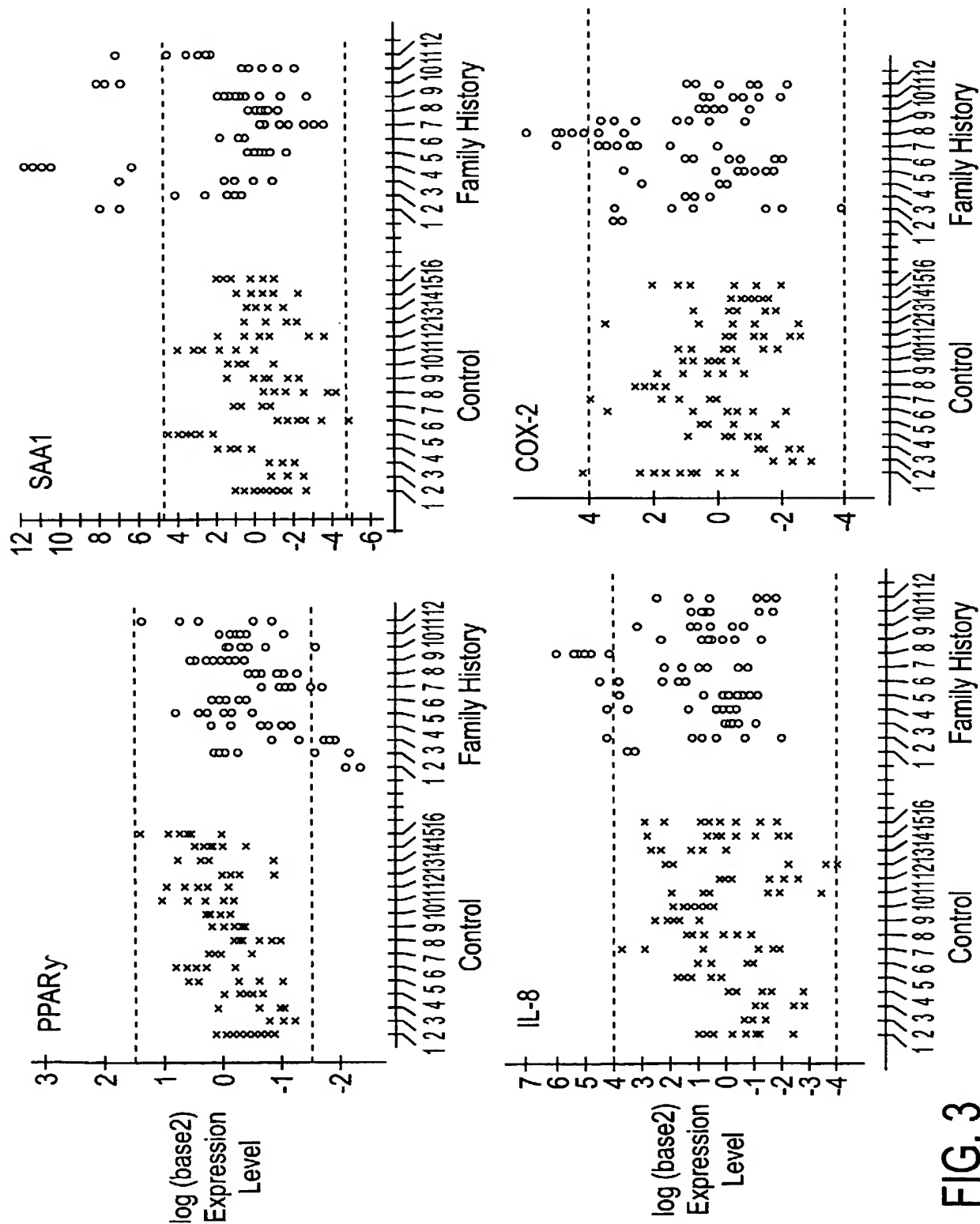


FIG. 3

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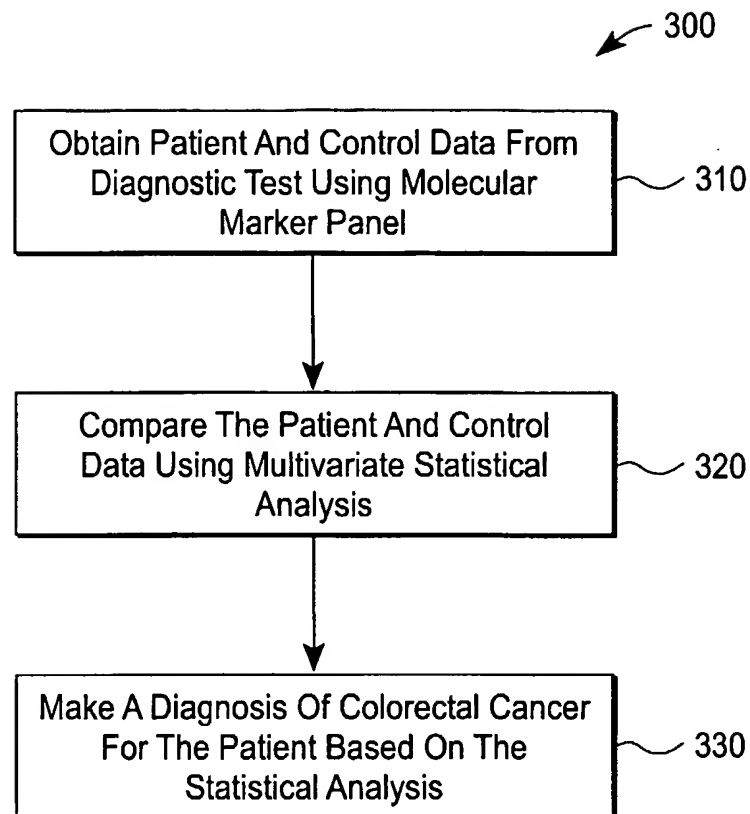


FIG. 5

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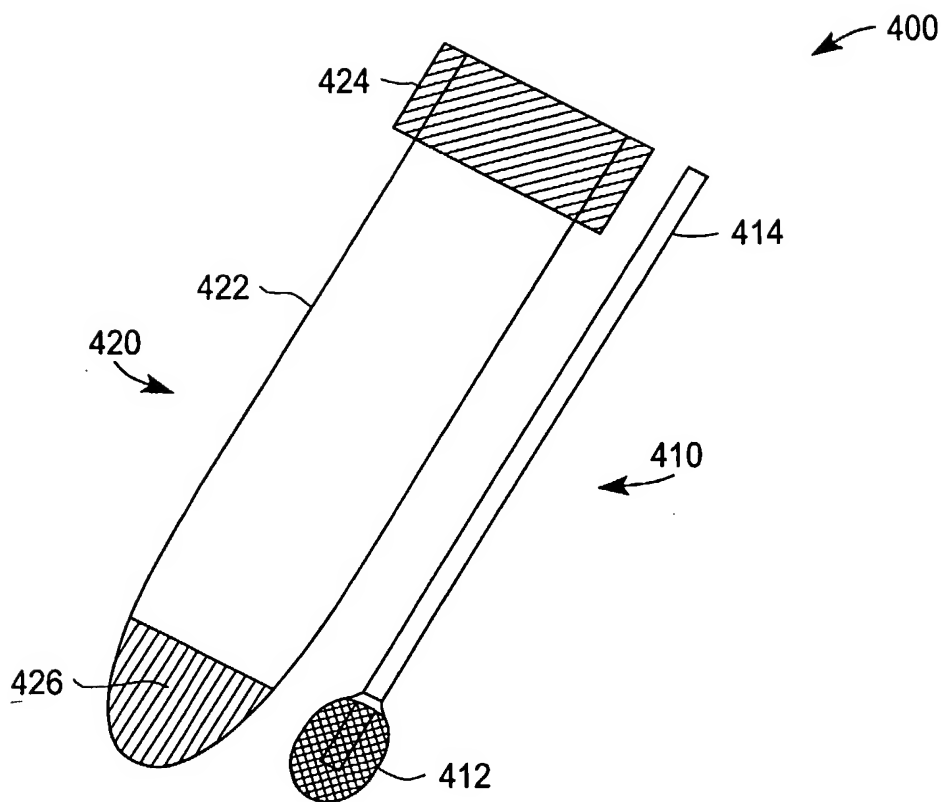


FIG. 6

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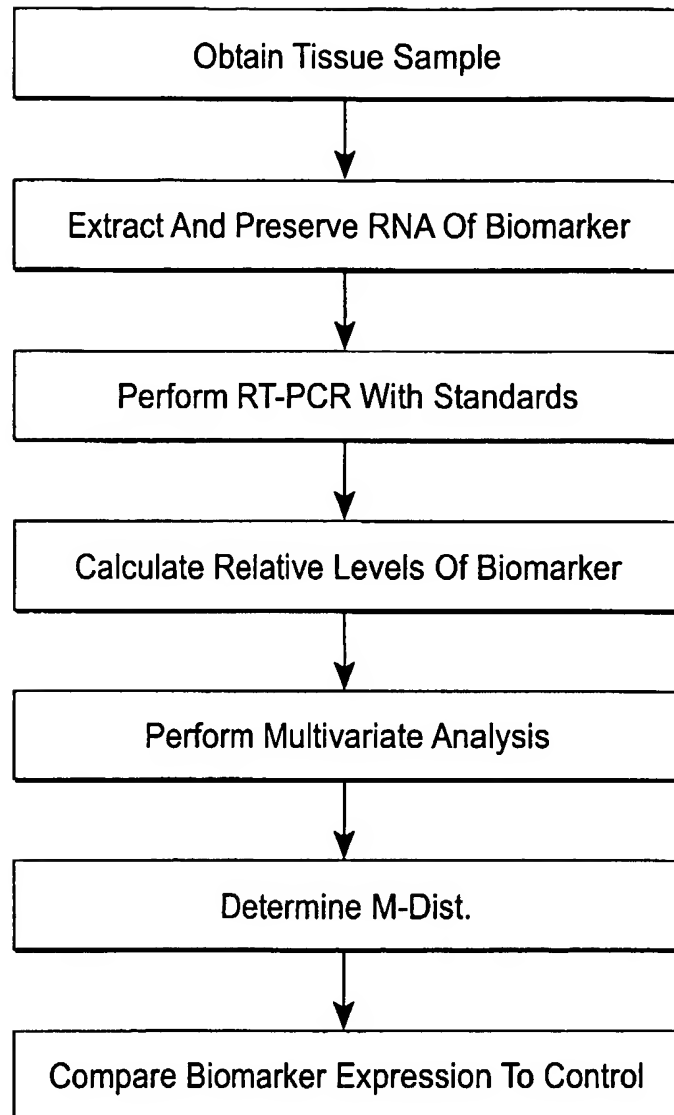


FIG. 7

10/10

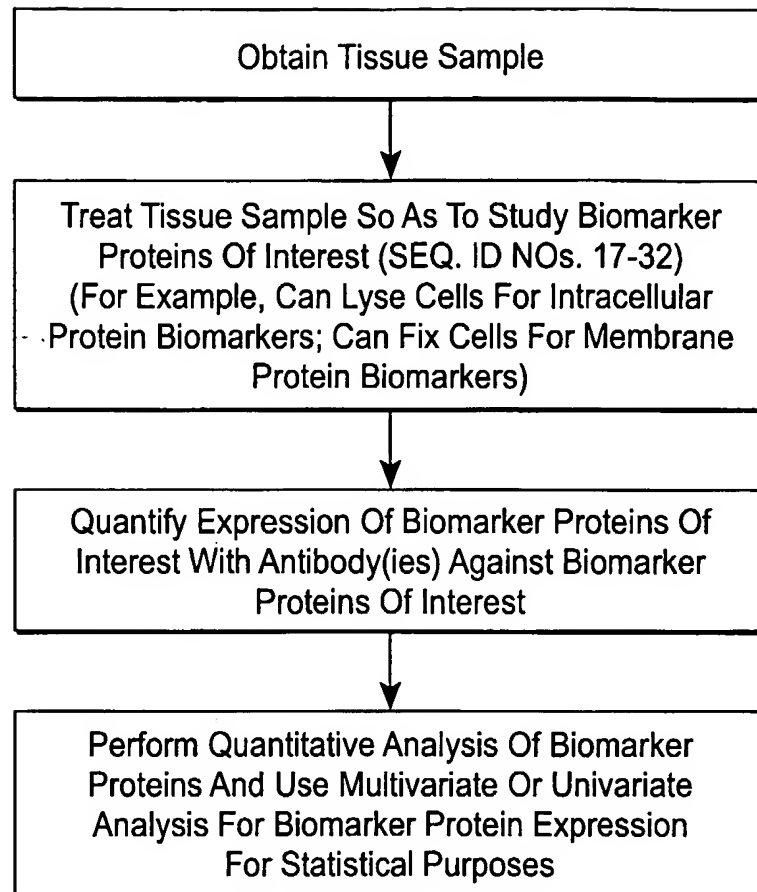


FIG. 8

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EQUENCE LISTING

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:120> DRUG SCREENING AND MOLECULAR DIAGNOSTIC TEST FOR EARLY DETECTION
      OF COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF
:130> NLEE-01001W00 MCF/MLB
:150> 60/614,746
:151> 2004-09-30
:150> 60/651,344
:151> 2005-02-08
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 <213> HUMAN

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 <213> HUMAN

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 <211> 1850
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<213> HUMAN

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<210> 13
<211> 3301
<212> DNA
<213> HUMAN

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NLEE01001W00.ST25.txt

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 <213> HUMAN

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gttcatagaa	gggcacgtgg
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aactccatct	gtgcagcaaa
caacacaggg	gtgtacatcc
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atacagaacg	aatcctgaag
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gaaccaggac	tggaccagct
1140	

NLEE01001W00.ST25.txt

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NLEE01001W00.ST25.txt

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3083

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 <212> DNA
 <213> HUMAN

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NLEE01001W00.ST25.txt

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<211> 369
<212> DNA
<213> HUMAN

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gatgctgcca aaaggggacc tgggggtgtc tgggctgcag aagcgatcag cgatgccaga 240
gagaatatcc agagattctt tggccatggg gcggaggact cgctggctga tcaggctgcc 300
aatgaatggg gcaggagtgg caaagacccc aatcacttcc gacctgctgg cctgcctgag 360
aaatactga 369

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<210> 17
<211> 67
<212> PRT
<213> HUMAN

<400> 17

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NLEE01001w00.ST25.txt

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Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
      35              40              45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
      50              55              60
Glu Ile Met
65

<210> 18
<211> 604
<212> PRT
<213> HUMAN

<400> 18
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Thr Ala Asn Pro Cys Cys Ser His Pro Cys Gln Asn Arg Gly Val Cys
      20              25              30
Met Ser Val Gly Phe Asp Gln Tyr Lys Cys Asp Cys Thr Arg Thr Gly
      35              40              45
Phe Tyr Gly Glu Asn Cys Ser Thr Pro Glu Phe Leu Thr Arg Ile Lys
      50              55              60
Leu Phe Leu Lys Pro Thr Pro Asn Thr Val His Tyr Ile Leu Thr His
      65              70              75              80
Phe Lys Gly Phe Trp Asn Val Val Asn Asn Ile Pro Phe Leu Arg Asn
      85              90              95
Ala Ile Met Ser Tyr Val Leu Thr Ser Arg Ser His Leu Ile Asp Ser
      100              105              110
Pro Pro Thr Tyr Asn Ala Asp Tyr Gly Tyr Lys Ser Trp Glu Ala Phe
      115              120              125
Ser Asn Leu Ser Tyr Tyr Thr Arg Ala Leu Pro Pro Val Pro Asp Asp
      130              135              140
Cys Pro Thr Pro Leu Gly Val Lys Gly Lys Lys Gln Leu Pro Asp Ser

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NLEE01001wo0.ST25.txt

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				Leu	Leu	Leu
				Arg	Arg	Lys
				170		
				Phe	Ile	Pro
						175
Pro	Gln	Gly	Ser	Asn	Met	Met
			180			
				Phe	Ala	Phe
				185		
				Phe	Ala	Gln
						190
				His	Phe	Thr
His	Gln	Phe	Phe	Lys	Thr	Asp
		195				
				His	Lys	Arg
				200		
				Gly	Pro	Ala
						205
				Phe	Thr	Asn
Gly	Leu	Gly	His	Gly	Val	Asp
	210					215
				Leu	Asn	His
						Ile
						220
				Tyr	Gly	Glu
						Thr
						Leu
Ala	Arg	Gln	Arg	Lys	Leu	Arg
					230	
				Leu	Phe	Lys
						235
				Asp	Gly	Lys
						Met
						Lys
						240
Gln	Ile	Ile	Asp	Gly	Glu	Met
				245		
				Tyr	Pro	Pro
						250
				Thr	Val	Lys
						255
				Asp	Thr	Gln
Ala	Glu	Met	Ile	Tyr	Pro	Pro
			260			
				Gln	Val	Pro
					265	
				Pro	Glu	His
						270
				Leu	Arg	Phe
						Ala
Val	Gly	Gln	Glu	Val	Phe	Gly
		275				
				Leu	Val	Pro
					280	
				Pro	Gly	Leu
						285
				Met	Met	Tyr
						Ala
Thr	Ile	Trp	Leu	Arg	Glu	His
	290					295
				Asn	Arg	Val
						Cys
						300
				Asp	Val	Leu
						Lys
						Gln
Glu	His	Pro	Glu	Trp	Gly	Asp
					310	
				Glu	Gln	Leu
						Phe
						315
				Gln	Thr	Ser
						Arg
						Leu
						320
Ile	Leu	Ile	Gly	Glu	Thr	Ile
						Lys
						Ile
						Val
						330
				Ile	Glu	Asp
						Tyr
						Val
						335
His	Leu	Ser	Gly	Tyr	His	Phe
			340			
				Lys	Leu	Lys
					345	
				Phe	Asp	Pro
						350
				Glu	Leu	Leu
Phe	Asn	Lys	Gln	Phe	Gln	Tyr
		355				
				Gln	Asn	Arg
						360
				Ile	Ala	Ala
						365
				Glu	Phe	Asn
Thr	Leu	Tyr	His	Trp	His	Pro
	370					375
				Leu	Leu	Pro
						Asp
						380
				Phe	Gln	Ile
						His
Asp	Gln	Lys	Tyr	Asn	Tyr	Gln
					390	
				Gln	Gln	Phe
						Ile
						Tyr
						395
				Asn	Asn	Ser
						Ile
						Leu
						400

NLEE01001W00.ST25.txt

Leu Glu His Gly Ile Thr Gln Phe Val Glu Ser Phe Thr Arg Gln Ile
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Ala Gly Arg Val Ala Gly Gly Arg Asn Val Pro Pro Ala Val Gln Lys
 420 425 430

Val Ser Gln Ala Ser Ile Asp Gln Ser Arg Gln Met Lys Tyr Gln Ser
 435 440 445

Phe Asn Glu Tyr Arg Lys Arg Phe Met Leu Lys Pro Tyr Glu Ser Phe
 450 455 460

Glu Glu Leu Thr Gly Glu Lys Glu Met Ser Ala Glu Leu Glu Ala Leu
 465 470 475 480

Tyr Gly Asp Ile Asp Ala Val Glu Leu Tyr Pro Ala Leu Leu Val Glu
 485 490 495

Lys Pro Arg Pro Asp Ala Ile Phe Gly Glu Thr Met Val Glu Val Gly
 500 505 510

Ala Pro Phe Ser Leu Lys Gly Leu Met Gly Asn Val Ile Cys Ser Pro
 515 520 525

Ala Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Gln Ile
 530 535 540

Ile Asn Thr Ala Ser Ile Gln Ser Leu Ile Cys Asn Asn Val Lys Gly
 545 550 555 560

Cys Pro Phe Thr Ser Phe Ser Val Pro Asp Pro Glu Leu Ile Lys Thr
 565 570 575

Val Thr Ile Asn Ala Ser Ser Ser Arg Ser Gly Leu Asp Asp Ile Asn
 580 585 590

Pro Thr Val Leu Leu Lys Glu Arg Ser Thr Glu Leu
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<210> 19
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 <212> PRT
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<400> 19

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NLEE01001WO0.ST25.txt

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Leu Leu Asp Ala Ala Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys
 35 40 45

Tyr Phe Val Val Ile Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu
 50 55 60

Gly Asn Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg
 65 70 75 80

Ser Val Thr Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu
 85 90 95

Phe Ala Leu Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp
 100 105 110

Ile Phe Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val
 115 120 125

Asn Phe Tyr Ser Gly Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg
 130 135 140

Tyr Leu Ala Ile Val His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr
 145 150 155 160

Leu Val Lys Phe Ile Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu
 165 170 175

Ala Leu Pro Val Leu Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val
 180 185 190

Ser Pro Ala Cys Tyr Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg
 195 200 205

Met Leu Leu Arg Ile Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu
 210 215 220

Leu Ile Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys
 225 230 235 240

Ala His Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala Val
 245 250 255

Val Leu Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu
 260 265 270

NLEE01001W00.ST25.txt

Ala Asp Thr Leu Met Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg
 275 280 285

Arg Asn His Ile Asp Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile
 290 295 300

Leu His Ser Cys Leu Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys
 305 310 315 320

Phe Arg His Gly Leu Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser
 325 330 335

Lys Asp Ser Leu Pro Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser
 340 345 350

Ser Gly His Thr Ser Thr Thr Leu
 355 360

<210> 20
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 <212> PRT
 <213> HUMAN

<400> 20

Met Thr Ala Pro Gly Ala Ala Gly Arg Cys Pro Pro Thr Thr Trp Leu
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Gly Ser Leu Leu Leu Val Cys Leu Leu Ala Ser Arg Ser Ile Thr
 20 25 30

Glu Glu Val Ser Glu Tyr Cys Ser His Met Ile Gly Ser Gly His Leu
 35 40 45

Gln Ser Leu Gln Arg Leu Ile Asp Ser Gln Met Glu Thr Ser Cys Gln
 50 55 60

Ile Thr Phe Glu Phe Val Asp Gln Glu Gln Leu Lys Asp Pro Val Cys
 65 70 75 80

Tyr Leu Lys Lys Ala Phe Leu Leu Val Gln Asp Ile Met Glu Asp Thr
 85 90 95

Met Arg Phe Arg Asp Asn Thr Ala Asn Pro Ile Ala Ile Val Gln Leu
 100 105 110

Gln Glu Leu Ser Leu Arg Leu Lys Ser Cys Phe Thr Lys Asp Tyr Glu
 115 120 125

NLEE01001WO0.ST25.txt

Glu His Asp Lys Ala Cys Val Arg Thr Phe Tyr Glu Thr Pro Leu Gln
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 Leu Leu Glu Lys Val Lys Asn Val Phe Asn Glu Thr Lys Asn Leu Leu
 145 150 155 160
 Asp Lys Asp Trp Asn Ile Phe Ser Lys Asn Cys Asn Asn Ser Phe Ala
 165 170 175
 Glu Cys Ser Ser Gln Asp Val Val Thr Lys Pro Asp Cys Asn Cys Leu
 180 185 190
 Tyr Pro Lys Ala Ile Pro Ser Ser Asp Pro Ala Ser Val Ser Pro His
 195 200 205
 Gln Pro Leu Ala Pro Ser Met Ala Pro Val Ala Gly Leu Thr Trp Glu
 210 215 220
 Asp Ser Glu Gly Thr Glu Gly Ser Ser Leu Leu Pro Gly Glu Gln Pro
 225 230 235 240
 Leu His Thr Val Asp Pro Gly Ser Ala Lys Gln Arg Pro Pro Arg Ser
 245 250 255
 Thr Cys Gln Ser Phe Glu Pro Pro Glu Thr Pro Val Val Lys Asp Ser
 260 265 270
 Thr Ile Gly Gly Ser Pro Gln Pro Arg Pro Ser Val Gly Ala Phe Asn
 275 280 285
 Pro Gly Met Glu Asp Ile Leu Asp Ser Ala Met Gly Thr Asn Trp Val
 290 295 300
 Pro Glu Glu Ala Ser Gly Glu Ala Ser Glu Ile Pro Val Pro Gln Gly
 305 310 315 320
 Thr Glu Leu Ser Pro Ser Arg Pro Gly Gly Gly Ser Met Gln Thr Glu
 325 330 335
 Pro Ala Arg Pro Ser Asn Phe Leu Ser Ala Ser Ser Pro Leu Pro Ala
 340 345 350
 Ser Ala Lys Gly Gln Gln Pro Ala Asp Val Thr Ala Thr Ala Leu Pro
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 Arg Val Gly Pro Val Met Pro Thr Gly Gln Asp Trp Asn His Thr Pro
 370 375 380

NLEE01001wo0.ST25.txt

Gln Lys Thr Asp His Pro Ser Ala Leu Leu Arg Asp Pro Pro Glu Pro
 385 390 395 400

Gly Ser Pro Arg Ile Ser Ser Leu Arg Pro Gln Ala Leu Ser Asn Pro
 405 410 415

Ser Thr Leu Ser Ala Gln Pro Gln Leu Ser Arg Ser His Ser Ser Gly
 420 425 430

Ser Val Leu Pro Leu Gly Glu Leu Glu Gly Arg Arg Ser Thr Arg Asp
 435 440 445

Arg Thr Ser Pro Ala Glu Pro Glu Ala Ala Pro Ala Ser Glu Gly Ala
 450 455 460

Ala Arg Pro Leu Pro Arg Phe Asn Ser Val Pro Leu Thr Asp Thr Gly
 465 470 475 480

His Glu Arg Gln Ser Glu Gly Ser Ser Ser Pro Gln Leu Gln Glu Ser
 485 490 495

Val Phe His Leu Leu Val Pro Ser Val Ile Leu Val Leu Leu Ala Val
 500 505 510

Gly Gly Leu Leu Phe Tyr Arg Trp Arg Arg Arg Ser His Gln Glu Pro
 515 520 525

Gln Arg Ala Asp Ser Pro Leu Glu Gln Pro Glu Gly Ser Pro Leu Thr
 530 535 540

Gln Asp Asp Arg Gln Val Glu Leu Pro Val
 545 550

<210> 21
 <211> 107
 <212> PRT
 <213> HUMAN

<400> 21

Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15

Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
 20 25 30

Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35 40 45

NLEE01001W00.ST25.txt

Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
 50 55 60

Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65 70 75 80

Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
 85 90 95

Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
 100 105

<210> 22
 <211> 106
 <212> PRT
 <213> HUMAN

<400> 22

Met Ala His Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15

Arg Val Ala Leu Leu Leu Leu Leu Val Gly Ser Arg Arg Ala Ala
 20 25 30

Gly Ala Ser Val Val Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu
 35 40 45

Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Asn Val Arg Ser Pro
 50 55 60

Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly
 65 70 75 80

Lys Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln Lys Ile Ile
 85 90 95

Glu Lys Ile Leu Asn Lys Gly Ser Thr Asn
 100 105

<210> 23
 <211> 300
 <212> PRT
 <213> HUMAN

<400> 23

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1 5 10 15

NLEE01001W00.ST25.txt

Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20 25 30
 Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35 40 45
 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
 50 55 60
 Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
 65 70 75 80
 Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
 85 90 95
 Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
 100 105 110
 Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
 115 120 125
 Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
 130 135 140
 Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
 145 150 155 160
 Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
 165 170 175
 Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
 180 185 190
 Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
 195 200 205
 Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
 210 215 220
 Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
 225 230 235 240
 Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
 245 250 255
 Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
 260 265 270

NLEE01001WO0.ST25.txt

Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
 275 280 285

Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
 290 295 300

<210> 24
 <211> 295
 <212> PRT
 <213> HUMAN

<400> 24

Met Glu His Gln Leu Leu Cys Cys Glu Val Glu Thr Ile Arg Arg Ala
 1 5 10 15

Tyr Pro Asp Ala Asn Leu Leu Asn Asp Arg Val Leu Arg Ala Met Leu
 20 25 30

Lys Ala Glu Glu Thr Cys Ala Pro Ser Val Ser Tyr Phe Lys Cys Val
 35 40 45

Gln Lys Glu Val Leu Pro Ser Met Arg Lys Ile Val Ala Thr Trp Met
 50 55 60

Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu
 65 70 75 80

Ala Met Asn Tyr Leu Asp Arg Phe Leu Ser Leu Glu Pro Val Lys Lys
 85 90 95

Ser Arg Leu Gln Leu Leu Gly Ala Thr Cys Met Phe Val Ala Ser Lys
 100 105 110

Met Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr
 115 120 125

Asp Gly Ser Ile Arg Pro Glu Glu Leu Leu Gln Met Glu Leu Leu Leu
 130 135 140

Val Asn Lys Leu Lys Trp Asn Leu Ala Ala Met Thr Pro His Asp Phe
 145 150 155 160

Ile Glu His Phe Leu Ser Lys Met Pro Glu Ala Glu Glu Asn Lys Gln
 165 170 175

Ile Ile Arg Lys His Ala Gln Thr Phe Val Ala Ser Cys Ala Thr Asp
 180 185 190

NLEE01001W00.ST25.txt

Val Lys Phe Ile Ser Asn Pro Pro Ser Met Val Ala Ala Gly Ser Val
 195 200 205
 Val Ala Ala Val Gln Gly Leu Asn Leu Arg Ser Pro Asn Asn Phe Leu
 210 215 220
 Ser Tyr Tyr Arg Leu Thr Arg Phe Leu Ser Arg Val Ile Lys Cys Asp
 225 230 235 240
 Pro Asp Cys Leu Arg Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Glu
 245 250 255
 Ser Ser Leu Arg Gln Ala Gln Gln Asn Met Asp Pro Lys Ala Ala Glu
 260 265 270
 Glu Glu Glu Glu Glu Glu Glu Val Asp Leu Ala Cys Thr Pro Thr
 275 280 285
 Asp Val Arg Asp Val Asp Ile
 290 295

<210> 25
 <211> 439
 <212> PRT
 <213> HUMAN

<400> 25

Met Pro Leu Asn Val Ser Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr
 1 5 10 15
 Asp Ser Val Gln Pro Tyr Phe Tyr Cys Asp Glu Glu Glu Asn Phe Tyr
 20 25 30
 Gln Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp
 35 40 45
 Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser
 50 55 60
 Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Thr Pro Phe
 65 70 75 80
 Ser Leu Arg Gly Asp Asn Asp Gly Gly Gly Gly Ser Phe Ser Thr Ala
 85 90 95
 Asp Gln Leu Glu Met Val Thr Glu Leu Leu Gly Gly Asp Met Val Asn
 100 105 110

NLEE01001WO0.ST25.txt

Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile Lys Asn Ile
 115 120 125
 Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala Ala Lys Leu
 130 135 140
 Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys Asp Ser Gly
 145 150 155 160
 Ser Pro Asn Pro Ala Arg Gly His Ser Val Cys Ser Thr Ser Ser Leu
 165 170 175
 Tyr Leu Gln Asp Leu Ser Ala Ala Ala Ser Glu Cys Ile Asp Pro Ser
 180 185 190
 Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro Lys Ser Cys
 195 200 205
 Ala Ser Gln Asp Ser Ser Ala Phe Ser Pro Ser Ser Asp Ser Leu Leu
 210 215 220
 Ser Ser Thr Glu Ser Ser Pro Gln Gly Ser Pro Glu Pro Leu Val Leu
 225 230 235 240
 His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln
 245 250 255
 Glu Asp Glu Glu Glu Ile Asp Val Val Ser Val Glu Lys Arg Gln Ala
 260 265 270
 Pro Gly Lys Arg Ser Glu Ser Gly Ser Pro Ser Ala Gly Gly His Ser
 275 280 285
 Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg Cys His Val Ser Thr
 290 295 300
 His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro
 305 310 315 320
 Ala Ala Lys Arg Val Lys Leu Asp Ser Val Arg Val Leu Arg Gln Ile
 325 330 335
 Ser Asn Asn Arg Lys Cys Thr Ser Pro Arg Ser Ser Asp Thr Glu Glu
 340 345 350
 Asn Val Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn

33

NLEE01001W00.ST25.txt

130

135

140

Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
 145 150 155 160

Lys Arg Lys Pro

<210> 27
 <211> 468
 <212> PRT
 <213> HUMAN

<400> 27

Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
 1 5 10 15

Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
 20 25 30

Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
 35 40 45

Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
 50 55 60

Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
 65 70 75 80

Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
 85 90 95

Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
 100 105 110

His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
 115 120 125

Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
 130 135 140

Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
 145 150 155 160

Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
 165 170 175

Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu

NLEE01001W00.ST25.txt

180 185 190

His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
195 200 205

Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
210 215 220

Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
225 230 235 240

Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
245 250 255

Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
260 265 270

Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
275 280 285

Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
290 295 300

Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
305 310 315 320

Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
325 330 335

Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
340 345 350

Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
355 360 365

Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
370 375 380

Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
385 390 395 400

Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
405 410 415

Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
420 425 430

NLEE01001W00.ST25.txt

Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
 435 440 445

Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
 450 455 460

Arg Asp Met Tyr
 465

<210> 28
 <211> 505
 <212> PRT
 <213> HUMAN

<400> 28

Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
 1 5 10 15

Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
 20 25 30

Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
 35 40 45

Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
 50 55 60

Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
 65 70 75 80

Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp
 85 90 95

Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser
 100 105 110

Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
 115 120 125

Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
 130 135 140

Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
 145 150 155 160

Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
 165 170 175

NLEE01001W00.ST25.txt

Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
 180 185 190
 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
 195 200 205
 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
 210 215 220
 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
 225 230 235 240
 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
 245 250 255
 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
 260 265 270
 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
 275 280 285
 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
 290 295 300
 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
 305 310 315 320
 Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
 325 330 335
 Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
 340 345 350
 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
 355 360 365
 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
 370 375 380
 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
 385 390 395 400
 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
 405 410 415
 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
 420 425 430

NLEE01001w00.ST25.txt

Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
 435 440 445

Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
 450 455 460

Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
 465 470 475 480

Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
 485 490 495

Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
 500 505

<210> 29
 <211> 441
 <212> PRT
 <213> HUMAN

<400> 29

Met Glu Gln Pro Gln Glu Glu Ala Pro Glu Val Arg Glu Glu Glu Glu
 1 5 10 15

Lys Glu Glu Val Ala Glu Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly
 20 25 30

Pro Gln His Ala Leu Pro Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser
 35 40 45

Ser Ser Pro Pro Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly
 50 55 60

Ala Ser Cys Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys
 65 70 75 80

Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly
 85 90 95

Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu
 100 105 110

Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys
 115 120 125

Arg Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg
 130 135 140

NLEE01001w00.ST25.txt

Phe Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu
 145 150 155 160
 Thr Ala Asn Glu Gly Ser Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys
 165 170 175
 Ala Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met
 180 185 190
 Thr Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ala Ser His Thr
 195 200 205
 Ala Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys
 210 215 220
 Gly Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu
 225 230 235
 Ile Ser Val His Val Phe Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr
 245 250 255
 Val Arg Glu Leu Thr Glu Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser
 260 265 270
 Leu Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
 275 280 285
 Ala Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu
 290 295 300
 Val Ala Asn Gly Ser Gly Phe Val Thr Arg Glu Phe Leu Arg Ser Leu
 305 310 315 320
 Arg Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val
 325 330 335
 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile
 340 345 350
 Ala Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro
 355 360 365
 Arg Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His
 370 375 380
 Leu Gln Ala Asn His Pro Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu
 385 390 395 400

NLEE01001W00.ST25.txt

Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
 405 410 415

Met Gln Arg Ile Lys Lys Thr Glu Thr Glu Thr Ser Leu His Pro Leu
 420 425 430

Leu Gln Glu Ile Tyr Lys Asp Met Tyr
 435 440

<210> 30
 <211> 742
 <212> PRT
 <213> HUMAN

<400> 30

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
 1 5 10 15

Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30

Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
 35 40 45

Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
 50 55 60

Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80

Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95

Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Ser Asn Thr Ser
 100 105 110

Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125

Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140

Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160

Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175

NLEE01001w00.ST25.txt

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Thr Leu
 210 215 220
 Met Ser Thr Ser Ala Thr Ala Thr Glu Thr Ala Thr Lys Arg Gln Glu
 225 230 235 240
 Thr Trp Asp Trp Phe Ser Trp Leu Phe Leu Pro Ser Glu Ser Lys Asn
 245 250 255
 His Leu His Thr Thr Thr Gln Met Ala Gly Thr Ser Ser Asn Thr Ile
 260 265 270
 Ser Ala Gly Trp Glu Pro Asn Glu Glu Asn Glu Asp Glu Arg Asp Arg
 275 280 285
 His Leu Ser Phe Ser Gly Ser Gly Ile Asp Asp Asp Glu Asp Phe Ile
 290 295 300
 Ser Ser Thr Ile Ser Thr Thr Pro Arg Ala Phe Asp His Thr Lys Gln
 305 310 315 320
 Asn Gln Asp Trp Thr Gln Trp Asn Pro Ser His Ser Asn Pro Glu Val
 325 330 335
 Leu Leu Gln Thr Thr Thr Arg Met Thr Asp Val Asp Arg Asn Gly Thr
 340 345 350
 Thr Ala Tyr Glu Gly Asn Trp Asn Pro Glu Ala His Pro Pro Leu Ile
 355 360 365
 His His Glu His His Glu Glu Glu Glu Thr Pro His Ser Thr Ser Thr
 370 375 380
 Ile Gln Ala Thr Pro Ser Ser Thr Thr Glu Glu Thr Ala Thr Gln Lys
 385 390 395 400
 Glu Gln Trp Phe Gly Asn Arg Trp His Glu Gly Tyr Arg Gln Thr Pro
 405 410 415
 Lys Glu Asp Ser His Ser Thr Thr Gly Thr Ala Ala Ala Ser Ala His
 41

NLEE01001wo0.ST25.txt

420

425

430

Thr Ser His Pro Met Gln Gly Arg Thr Thr Pro Ser Pro Glu Asp Ser
 435 440 445

Ser Trp Thr Asp Phe Phe Asn Pro Ile Ser His Pro Met Gly Arg Gly
 450 455 460

His Gln Ala Gly Arg Arg Met Asp Met Asp Ser Ser His Ser Ile Thr
 465 470 475 480

Leu Gln Pro Thr Ala Asn Pro Asn Thr Gly Leu Val Glu Asp Leu Asp
 485 490 495

Arg Thr Gly Pro Leu Ser Met Thr Thr Gln Gln Ser Asn Ser Gln Ser
 500 505 510

Phe Ser Thr Ser His Glu Gly Leu Glu Glu Asp Lys Asp His Pro Thr
 515 520 525

Thr Ser Thr Leu Thr Ser Ser Asn Arg Asn Asp Val Thr Gly Gly Arg
 530 535 540

Arg Asp Pro Asn His Ser Glu Gly Ser Thr Thr Leu Leu Glu Gly Tyr
 545 550 555 560

Thr Ser His Tyr Pro His Thr Lys Glu Ser Arg Thr Phe Ile Pro Val
 565 570 575

Thr Ser Ala Lys Thr Gly Ser Phe Gly Val Thr Ala Val Thr Val Gly
 580 585 590

Asp Ser Asn Ser Asn Val Asn Arg Ser Leu Ser Gly Asp Gln Asp Thr
 595 600 605

Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu Ser Asp
 610 615 620

Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr Ser Gly
 625 630 635 640

Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu Ala Ser
 645 650 655

Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val Asn Ser
 660 665 670

NLEE01001W00.ST25.txt

Arg Arg Arg Cys Gly Gln Lys Lys Lys Leu Val Ile Asn Ser Gly Asn
 675 680 685

Gly Ala Val Glu Asp Arg Lys Pro Ser Gly Leu Asn Gly Glu Ala Ser
 690 695 700

Lys Ser Gln Glu Met Val His Leu Val Asn Lys Glu Ser Ser Glu Thr
 705 710 715 720

Pro Asp Gln Phe Met Thr Ala Asp Glu Thr Arg Asn Leu Gln Asn Val
 725 730 735

Asp Met Lys Ile Gly Val
 740

<210> 31
 <211> 489
 <212> PRT
 <213> HUMAN

<400> 31

Met Leu Met Arg Leu Val Leu Thr Val Arg Ser Asn Leu Ile Pro Ser
 1 5 10 15

Pro Pro Thr Tyr Asn Ser Ala His Asp Tyr Ile Ser Trp Glu Ser Phe
 20 25 30

Ser Asn Val Ser Tyr Tyr Thr Arg Ile Leu Pro Ser Val Pro Lys Asp
 35 40 45

Cys Pro Thr Pro Met Gly Thr Lys Gly Lys Lys Gln Leu Pro Asp Ala
 50 55 60

Gln Leu Leu Ala Arg Arg Phe Leu Leu Arg Arg Lys Phe Ile Pro Asp
 65 70 75 80

Pro Gln Gly Thr Asn Leu Met Phe Ala Phe Phe Ala Gln His Phe Thr
 85 90 95

His Gln Phe Phe Lys Thr Ser Gly Lys Met Gly Pro Gly Phe Thr Lys
 100 105 110

Ala Leu Gly His Gly Val Asp Leu Gly His Ile Tyr Gly Asp Asn Leu
 115 120 125

Glu Arg Gln Tyr Gln Leu Arg Leu Phe Lys Asp Gly Lys Leu Lys Tyr
 130 135 140

NLEE01001W00.ST25.txt

Gln Val Leu Asp Gly Glu Met Tyr Pro Pro Ser Val Glu Glu Ala Pro
 145 150 155 160

Val Leu Met His Tyr Pro Arg Gly Ile Pro Pro Gln Ser Gln Met Ala
 165 170 175

Val Gly Gln Glu Val Phe Gly Leu Leu Pro Gly Leu Met Leu Tyr Ala
 180 185 190

Thr Leu Trp Leu Arg Glu His Asn Arg Val Cys Asp Leu Leu Lys Ala
 195 200 205

Glu His Pro Thr Trp Gly Asp Glu Gln Leu Phe Gln Thr Thr Arg Leu
 210 215 220

Ile Leu Ile Gly Glu Thr Ile Lys Ile Val Ile Glu Glu Tyr Val Gln
 225 230 235 240

Gln Leu Ser Gly Tyr Phe Leu Gln Leu Lys Phe Asp Pro Glu Leu Leu
 245 250 255

Phe Gly Val Gln Phe Gln Tyr Arg Asn Arg Ile Ala Met Glu Phe Asn
 260 265 270

His Leu Tyr His Trp His Pro Leu Met Pro Asp Ser Phe Lys Val Gly
 275 280 285

Ser Gln Glu Tyr Ser Tyr Glu Gln Phe Leu Phe Asn Thr Ser Met Leu
 290 295 300

Val Asp Tyr Gly Val Glu Ala Leu Val Asp Ala Phe Ser Arg Gln Ile
 305 310 315 320

Ala Gly Arg Ile Gly Gly Gly Arg Asn Met Asp His His Ile Leu His
 325 330 335

Val Ala Val Asp Val Ile Arg Glu Ser Arg Glu Met Arg Leu Gln Pro
 340 345 350

Phe Asn Glu Tyr Arg Lys Arg Phe Gly Met Lys Pro Tyr Thr Ser Phe
 355 360 365

Gln Glu Leu Val Gly Glu Lys Glu Met Ala Ala Glu Leu Glu Glu Leu
 370 375 380

Tyr Gly Asp Ile Asp Ala Leu Glu Phe Tyr Pro Gly Leu Leu Leu Glu
 385 390 395 400

NLEE01001WO0.ST25.txt

Lys Cys His Pro Asn Ser Ile Phe Gly Glu Ser Met Ile Glu Ile Gly
 405 410 415

Ala Pro Phe Ser Leu Lys Gly Leu Leu Gly Asn Pro Ile Cys Ser Pro
 420 425 430

Glu Tyr Trp Lys Pro Ser Thr Phe Gly Gly Glu Val Gly Phe Asn Ile
 435 440 445

Val Lys Thr Ala Thr Leu Lys Lys Leu Val Cys Leu Asn Thr Lys Thr
 450 455 460

Cys Pro Tyr Val Ser Phe Arg Val Pro Asp Ala Ser Gln Asp Asp Gly
 465 470 475 480

Pro Ala Val Glu Arg Pro Ser Thr Glu
 485

<210> 32
 <211> 122
 <212> PRT
 <213> HUMAN

<400> 32

Met Lys Leu Leu Thr Gly Leu Val Phe Cys Ser Leu Val Leu Gly Val
 1 5 10 15

Ser Ser Arg Ser Phe Phe Ser Phe Leu Gly Glu Ala Phe Asp Gly Ala
 20 25 30

Arg Asp Met Trp Arg Ala Tyr Ser Asp Met Arg Glu Ala Asn Tyr Ile
 35 40 45

Gly Ser Asp Lys Tyr Phe His Ala Arg Gly Asn Tyr Asp Ala Ala Lys
 50 55 60

Arg Gly Pro Gly Gly Val Trp Ala Ala Glu Ala Ile Ser Asp Ala Arg
 65 70 75 80

Glu Asn Ile Gln Arg Phe Phe Gly His Gly Ala Glu Asp Ser Leu Ala
 85 90 95

Asp Gln Ala Ala Asn Glu Trp Gly Arg Ser Gly Lys Asp Pro Asn His
 100 105 110

Phe Arg Pro Ala Gly Leu Pro Glu Lys Tyr
 115 120

NLEE01001WO0.ST25.txt

<210> 33
<211> 26
<212> DNA
<213> HUMAN

<400> 33
agatattgca cgggagaata tacaaa 26

<210> 34
<211> 27
<212> DNA
<213> HUMAN

<400> 34
tcaattcctg aaattaaagt tcggata 27

<210> 35
<211> 23
<212> DNA
<213> HUMAN

<400> 35
tctgcagagt tggaagcact cta 23

<210> 36
<211> 21
<212> DNA
<213> HUMAN

<400> 36
gccgaggctt ttctaccaga a 21

<210> 37
<211> 20
<212> DNA
<213> HUMAN

<400> 37
catggcttga tcagcaagga 20

<210> 38
<211> 21
<212> DNA
<213> HUMAN

<400> 38
tggaagtgtg ccctgaagaa g 21

<210> 39
<211> 21
<212> DNA
<213> HUMAN

<400> 39
aagcagcacc agcaagtga g 21

NLEE01001WO0.ST25.txt

<210> 40
<211> 21
<212> DNA
<213> HUMAN

<400> 40
tcatggcctg tgcagtcaa a 21

<210> 41
<211> 22
<212> DNA
<213> HUMAN

<400> 41
acatgccagc cactgtgata ga 22

<210> 42
<211> 21
<212> DNA
<213> HUMAN

<400> 42
ccctgccttc acaatgatct c 21

<210> 43
<211> 23
<212> DNA
<213> HUMAN

<400> 43
ggaattcacc tcaagaacat cca 23

<210> 44
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